

**FIGURE 1**

CTAAAAAATATGTTCTCTACAACACCAAGGCTCATTAAAAATATTTTAAATATT  
AATATACATTTCTTCTGTCAGAAATACATAAACTTTATTATATCAGCGCAGG  
5 GCGGCGCGGCGTCCGGTCCCGGGAGCAGAACCCGGCTTTTTCTTGGAGCGACG  
CTGTCTCTAGTCGCTGATCCCAAATGCACCGGCTCATCTTTGTCTACACTCTA  
ATCTGCGCAAACCTTTTGCAGCTGTCGGGACACTTCTGCAACCCCGCAGAGCG  
CATCCATCAAAGCTTTGCGCAACGCCAACCTCAGGCGAGATGAGAGCAATCA  
CCTCACAGACTTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGG  
10 CTACGTGCAGAGTCCTAGATTCCCGAACAGCTACCCAGGAACCTGCTCCTG  
ACATGGCGGCTTCACTCTCAGGAGAATACACGGATACAGCTAGTGTTTGACA  
ATCAGTTTGGATTAGAGGAAGCAGAAAATGATATCTGTAGGTATGATTTTGT  
GGAAGTTGAAGATATATCCGAAACCAGTACCATTATTAGAGGACGATGGTGT  
GGACACAAGGAAGTTCCTCCAAGGATAAAATCAAGAACGAACCAAATTA  
15 ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTTA  
TTATTCTTTGCTGGAAGATTTCCAACCCGCAGCAGCTTCAGAGACCAACTGGG  
AATCTGTCACAAGCTCTATTTCAAGGGGTATCCTATAACTCTCCATCAGTAACG  
GATCCCCTCTGATTGCGGATGCTCTGGACAAAAAATTGCAGAATTTGATA  
CAGTGGAAGATCTGCTCAAGTACTTCAATCCAGAGTCATGGCAAGAAGATCT  
20 TGAGAATATGTATCTGGACACCCCTCGGTATCGAGGCAGGTCATACCATGAC  
CGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTACA  
GTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGC  
CAATGTGGTCTTCTTTCCACGTTGCCTCCTCGTGCAGCGCTGTGGAGGAAATT  
GTGGCTGTGGAAGTGTCAACTGGAGGTCCTGCACATGCAATTCAGGGAAAAC  
25 CGTGAAAAAGTATCATGAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGG  
AGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCAGTTGGATCACCATG  
AACGA'GTGATTGTATCTGCAGCTCAAGACCACCTCGATAAGAGAATGTGCA  
CATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGAGGGTGAGATAAG  
AGACCCTTTTCCTACCAGCAACCAAACCTTACTACTAGCCTGCAATGCAATGAA  
30 CACAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAATGCCATGGCAAGTAGA  
AAGGTATATCATCAACTTCTATACCTAAGAATATAGGATTGCATTTAATAATA



## FIGURE 2

1 CTAAAAAATATGTTCTCTACAACACCAAGGCTCATTAAAAATATTT  
 46 TAAATATTAATATACATTTTCTTCTGTCAGAAATACATAAACTTT  
 5 91 ATTATATCAGCGCAGGGCGGCGGGCGTCGGTCCCGGGAGCAGAA  
 136 CCCGGCTTTTCTTGGAGCGACGCTGTCTCTAGTCGCTGATCCCA  
  
 181 AATGCACCGGCTCATCTTTGTCTACACTCTAATCTGCGCAAACCTT  
 MetHisArgLeuIlePheValTyrThrLeuIleCysAlaAsnPhe  
 10 226 TTGCAGCTGTCGGGACACTTCTGCAACCCCGCAGAGCGCATCCAT  
 CysSerCysArgAspThrSerAlaThrProGlnSerAlaSerIle  
  
 271 CAAAGCTTTGCGCAACGCCAACCTCAGGCGAGATGAGAGCAATCA  
 15 LysAlaLeuArgAsnAlaAsnLeuArgArgAspGluSerAsnHis  
 316 CCTCACAGACTTGTACCGAAGAGATGAGACCATCCAGGTGAAAGG  
 LeuThrAspLeuTyrArgArgAspGluThrIleGlnValLysGly  
  
 361 AAACGGCTACGTGCAGAGTCCTAGATTCCCGAACAGCTACCCAG  
 20 AsnGlyTyrValGlnSerProArgPheProAsnSerTyrProArg  
 406 GAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAATACACG  
 AsnLeuLeuLeuThrTrpArgLeuHisSerGlnGluAsnThrArg  
 25 451 GATACAGCTAGTGTGTTGACAATCAGTTTGGATTAGAGGAAGCAGA  
 IleGlnLeuValPheAspAsnGlnPheGlyLeuGluGluAlaGlu  
  
 496 AAATGATATCTGTAGGTATGATTTTGTGGAAGTTGAAGATATATC  
 30 AsnAspIleCysArgTyrAspPheValGluValGluAspIleSer  
 541 CGAAACCAGTACCATTATTAGAGGACGATGGTGTGGACACAAGGA  
 GluThrSerThrIleIleArgGlyArgTrpCysGlyHisLysGlu  
  
 586 AGTTCCTCCAAGGATAAAATCAAGAACGAACCAAATTAATCAC  
 35 ValProProArgIleLysSerArgThrAsnGlnIleLysIleThr  
 631 ATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGAT  
 PheLysSerAspAspTyrPheValAlaLysProGlyPheLysIle  
 40 676 TTATTATTCTTTGCTGGAAGATTTCCAACCCGCAGCAGCTTCAGA  
 TyrTyrSerLeuLeuGluAspPheGlnProAlaAlaAlaSerGlu

721 GACCAACTGGGAATCTGTCACAAGCTCTATTTTCAGGGGTATCCTA  
ThrAsnTrpGluSerValThrSerSerIleSerGlyValSerTyr

5 766 TAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGATGCTCT  
AsnSerProSerValThrAspProThrLeuIleAlaAspAlaLeu

811 GGACAAAAAATTGCAGAATTTGATACAGTGAAGATCTGCTCAA  
AspLysLysIleAlaGluPheAspThrValGluAspLeuLeuLys

10 856 GTACTTCAATCCAGAGTCATGGCAAGAAGATCTTGAGAATATGTA  
TyrPheAsnProGluSerTrpGlnGluAspLeuGluAsnMetTyr

15 901 TCTGGACACCCCTCGGTATCGAGGCAGGTCATACCATGACCGGAA  
LeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgLys

946 GTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTA  
SerLysValAspLeuAspArgLeuAsnAspAspAlaLysArgTyr

20 991 CAGTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAAGAGCT  
SerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeu

1036 GAAGTTGGCCAATGTGGTCTTCTTTCCACGTTGCCTCCTCGTGCA  
LysLeuAlaAsnValValPhePheProArgCysLeuLeuValGln

25 1081 GCGCTGTGGAGGAAATTGTGGCTGTGGAAGTGTCAACTGGAGGTC  
ArgCysGlyGlyAsnCysGlyCysGlyThrValAsnTrpArgSer

1126 CTGCACATGCAATTCAGGGAAAACCGTGAAAAAGTATCATGAGGT  
30 CysThrCysAsnSerGlyLysThrValLysLysTyrHisGluVal

1171 ATTACAGTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAA  
LeuGlnPheGluProGlyHisIleLysArgArgGlyArgAlaLys

35 1216 GACCATGGCTCTAGTTGACATCCAGTTGGATCACCATGAACGATG  
ThrMetAlaLeuValAspIleGlnLeuAspHisHisGluArgCys

1261 TGATTGTATCTGCAGCTCAAGACCACCTCGATAAGAGAATGTGCA  
AspCysIleCysSerSerArgProProArg (SEQ ID NO:12)

40 1306 CATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGAGGGTG  
1351 AGATAAGAGACCCTTTTCCTACCAGCAACCAAACCTTACTACTAGC  
1396 CTGCAATGCAATGAACACAAGTGGTTGCTGAGTCTCAGCCTTGCT



### FIGURE 3

A -- Cur2 1.6 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCC  
TGAGACTCTCCTGTGCAGCCTCTGGATTCAACTTCAGAACCTATAACATGAAC  
TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTA  
GTAGTAGTAGTAACATATACTACGCAGACTCAGTGAAGGGCCGATTACCAT  
CTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGA  
10 GCCGAGGACACGGCTGTATATTACTGTGCGAGAGATATTATGATTACGTTTG  
GGGAATTATCGCCTCGTTCTACTTTGACTACTGGGGCCAGGGAACCCTGGTC  
ACCGTCTCCTCAG (SEQ ID NO:55)

B -- Cur2 1.6 heavy chain amino acid sequence

15 EVQLVESGGGLVKPGGSLRLSCAASGFNFRITYNMNWVRQAPGKGLEWVSSISS  
SSNIYYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCARDIMITFGGIIAS  
FYFDYWGQGTLLVTVSS (SEQ ID NO:13)

20 C -- Cur2 1.6 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG  
TTTCAGCAGAAACCAGGGAAGCCCTAAGCGCCTGATCTATGCTGCATCCA  
25 GTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGA  
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT  
GTCTACAGCATAATAGTTACCCGCTCACTTTCGGCGGAGGGACCAAGGTGGA  
GATCAAAC (SEQ ID NO:56)

30 D -- Cur2 1.6 light chain amino acid sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWFQQKPGKAPKRLIYAASSLQ  
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGGTKVEIK (SEQ  
ID NO:14)

35

## FIGURE 4

A -- Cur2 1.11 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCTGGAGGAGGCTTGATCCAGCCTGGGGGGTCCC  
TGAGACTCTCCTGTGCAGCCTCTGGGTTACCGTCAGTAGCAACTACATGAGC  
TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGTTATTTATA  
GCGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGATTACCATCTC  
CAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCC  
10 GAGGACACGGCCGTGTATTACTGTGCGGGAACGGTGACTACGAATTACTACT  
ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAG (SEQ  
ID NO:57)

B -- Cur2 1.11 heavy chain amino acid sequence

15 EVQLVQSGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSG  
GSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAGTVTTNYYYGM  
DVWGQGTTVTVSS (SEQ ID NO:15)

C -- Cur2 1.11 light chain nucleotide sequence

20 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCCGTCACCCCTGGAGAGCC  
GGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCAAAGTAATGGATAC  
AACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGA  
TCTATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTCAAGTGGCAGT  
GGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATG  
25 TTGGGGTTTATTACTGCATGCAAGCTCTACAACTCTCACTTTCGGCGGAGGG  
ACCAAGGTGGAGATCAAAC (SEQ ID NO:58)

D -- Cur2 1.11 light chain amino acid sequence

30 DIVMTQSPLSLPVTGPGEPAISCRSSQSLLQSNQYNYLDWYLQKPGQSPQLLIYLG  
SNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTLTFGGGTKVEI  
K (SEQ ID NO:16)

## FIGURE 5

A -- Cur2 1.17 heavy chain nucleotide sequence

5

CAGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAAGTCCC  
TGAGACTCTCCTGTGCAGCGTCTGGATTACCTTCAGTAGCTATGGCATGCAC  
TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGT  
ATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCAT  
10 CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA  
GCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCAAGGATACAGATATG  
CTGGTTACTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT  
CACCGTCTCCTCAG (SEQ ID NO:59)

15 B -- Cur2 1.17 heavy chain protein sequence

QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIW  
YDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLR AEDTAVYYCARDQGYRYA  
GYYYDYGMDVWGQGT TVTSS (SEQ ID NO:17)

20

C -- Cur2 1.17 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG  
25 TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA  
GTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGA  
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT  
GTCTACAGCATAATAGTTACCCGCTCACTTTCGGCGGAGGGACCAAGGTGGA  
GATCAAAC (SEQ ID NO:60)

30

D -- Cur2 1.17 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ  
SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK (SEQ  
35 ID NO:18)



## **FIGURE 6**

A -- Cur2 1.18 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA  
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAA  
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA  
CCCAAACAGTGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACC  
10 ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA  
GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAGGGTATAGCAGTGGC  
TGGGACATACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACG  
GTCACCGTCTCCTCAG (SEQ ID NO:61)

15 B -- Cur2 1.18 heavy chain protein sequence

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM  
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAREGIAVAG  
TYYYYYGMDVWGQGTITVTVSS (SEQ D NO:19)

20 C -- Cur2 1.18 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG  
25 TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA  
GTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGA  
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTTCT  
GTCTACAGCATAATAGTTACCCATTCACTTTCGGCCCTGGGACCAAAGTGGAT  
ATCAAAC (SEQ ID NO:62)

30 D -- Cur2 1.18 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ  
SGVPSRFSGSGSGTEFTLTISSLQPEDFATYFCLQHNSYPFTFGPGTKVDIK (SEQ  
35 ID NO:20)

## FIGURE 7

### A -- Cur2 1.19 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAG  
TGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAAC  
TGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAAC  
CCTAACAGTGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACCA  
TGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAG  
10 ATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACGTTATGATTACGTTTG  
GGGGAGTTATCGTGCCTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT  
CACCGTCTCCTCAG (SEQ ID NO:63)

### B -- Cur2 1.19 heavy chain amino acid sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM  
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDVAVYYCARDVMITFG  
GVIVHYGMDVWGQGTTVTVSS (SEQ ID NO:21)

### C -- Cur2 1.19 light chain nucleotide sequence

20 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG  
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA  
25 GTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGA  
TTTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT  
GTCTACAGCATAATAGTGACCCGTGCAGTTTTGGCCAGGGGACCAAGCTGGA  
GATCAGAC (SEQ ID NO:64)

### D -- Cur2 1.19 light chain amino acid sequence

30 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ  
SGVPSRFSGSGSGTDFTLTISLQPEDFATYYCLQHNSDPCSFQGQGTKLEIR (SEQ  
ID NO:22)

35

## **FIGURE 8**

### **A -- Cur2 1.23 heavy chain nucleotide sequence**

5 GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCT  
CTGAAGATCTCCTGTGAGGGTTCTGGATACAGCTTTACCAGCTACTGGATCGG  
CTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATCATCTAT  
CCTGGTGA CTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCAGGTCACCA  
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA  
10 GGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGTATCGTATTACTATG  
TTTCGGGGAGTTATTATAACGTCCTTGACTACTGGGGCCAGGGAACCCTGGTC  
ACCGTCTCCTCAG (SEQ ID NO:65)

### **B -- Cur2 1.23 heavy chain amino acid sequence**

15 EVQLVQSGAEVKKPGESLKISCEGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPG  
DSDTRYSPSFQGVVISADKSISTAYLQWSSLKASDTAMYYCARHVSYYYVSGS  
YYNVFDYWGGQGLVTVSS (SEQ ID NO:23)

### **C -- Cur2 1.23 light chain nucleotide sequence**

20 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG  
TATCAGCAGATACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA  
GTTTGCAACGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGA  
ATTCCTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT  
25 GTCTACAGCATAATAGTTACCCGTGGACGTTTCGGCCAAGGGACCAAGGTGGA  
AATCAAAC (SEQ ID NO:66)

### **D -- Cur2 1.23 light chain amino acid sequence**

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQIPGKAPKRLIYAASSLQR  
30 GVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ  
ID NO:24)

## FIGURE 9

A -- Cur2 1.24.1 heavy chain nucleotide sequence

5

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC  
TGAGACTCTCCTGTGCAGCGTCTGGATTTCAGTTTCAGTAGCTATGGCATGCAC  
TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGATATATGGT  
ATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCAT  
10 CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA  
GCCGAGGACACGGCTGTGTATTATTGTGCGAGAGATCAGGGATACAGCTATG  
GTTACGTCTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT  
CACCGTCTCCTCAG (SEQ ID NO:67)

15 B -- Cur2 1.24.1 heavy chain protein sequence

QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQAPGKGLEWVADIW  
YDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQGYSYG  
YVYYDYGMDVWGQGTTVTVSS (SEQ ID NO:25)

20

C -- Cur2 1.24.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG  
25 TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA  
GTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGA  
GTTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT  
GTCTACAGCATAATAGTTACCCGTGGACGTTTCGGCCAAGGGACCAAGGTGGA  
AATCAAAC (SEQ ID NO:68)

30

D -- Cur2 1.24.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ  
SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ  
35 ID NO:26)

## FIGURE 10

A -- Cur2 1.25.1 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCGGGAGCAGAGGTGAAAAAGCCCGGGGAGTCT  
CTGAAGATCTCCTGTAAGGGTTCTGGATACAGGTTTACCAGCTACTGGATCGG  
CTGGGTGCGCCAGATGCCCCGGGAAAGGCCTGGAGTGGATGGGGATCATCTAT  
CCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCAGGTCACCA  
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA  
10 GGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGGATCGTATTATTATG  
GTTTCGGAGACTTATTATAATGTCTTTGACTACTGGGGCCAGGGAACCCTGGTC  
ACCGTCTCCTCAG (SEQ ID NO:69)

B -- Cur2 1.25.1 heavy chain protein sequence

15 EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPG  
DSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHGSYYYGSET  
YYNVFDYWGGTGLTVSS (SEQ ID NO:27)

20 C -- Cur2 1.25.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG  
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA  
25 GTTTGCAAAGTGGGGTCCCATCAAGGTTCAAGCGCAGTGGATCTGGGACAGA  
ATCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT  
GTCTACAGCATAATAGTTACCCGTGGACGTTTCGGCCAAGGGACCAAGGTGGA  
AATCAAAC (SEQ ID NO:70)

30 D -- Cur2 1.25.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ  
SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ  
ID NO:28)

35

## FIGURE 11

### A -- Cur2 1.29 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCGGGAGCAGAGGTGAAAAAGCCCGGGGAGTCT  
CTGAAGATCTCCTGTAAGGGTTCTGGATACAGCTTTACCAGCTACTGGATCGG  
CTGGGTGCGCCAGATGCCCCGGGAAAGGCCTGGAGTGGATGGGGATCATCTAT  
CCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCAGGCCACCA  
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA  
10 GGCCTCGGACACCGCCATGTATTACTGTGCGAGACACGTGGATGTAGGGGCT  
ACGATTGGGGGATATTACTATTACTACCACGGTATGGACGTCTGGGGCCAAG  
GGACCACGGTCACCGTCTCCTCAG (SEQ ID NO:71)

### B -- Cur2 1.29 heavy chain protein sequence

15 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPG  
DSDTRYSPSFQGQATISADKSISTAYLQWSSLKASDTAMY YCARHVDVGATIGG  
YYYYYHGMDVWGQGT VTVSS (SEQ ID NO:29)

### C -- Cur2 1.29 light chain nucleotide sequence

20 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCCGTCACCCCTGGAGAGCC  
GGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACA  
ACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAACCTCCTGATC  
25 TATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTCA GTGGCAGTGG  
ATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGACGATGTT  
GGGGTTTATTACTGCATGCAAGCTCTACAATCTCTCATGTGCAGTTTGGCCA  
GGGGACCAAGCTGGAGATCAAAC (SEQ ID NO:72)

### D -- Cur2 1.29 light chain protein sequence

30 DIVMTQSPLSLPVTGPGEPAISCRSSQSLLSNGYNYLDWYLQKPGQSPQLLIYLG  
SNRASGVPDFRSGSGSGTDFTLKISRVEADDVG VYYCMQALQSLMCSFGQGTKL  
EIK (SEQ ID NO:30)

35

## FIGURE 12

### A -- Cur2 1.33 heavy chain nucleotide sequence

5 CAGGTTTCAGCTGGTGCAGTCGGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAG  
TGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGCTATGGTATCAGC  
TGGGTGCGACAGGCCCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCG  
CTTACAATGGTAACACAAACTATGCACAGAAGCTCCAGGGCAGAGTCACCAT  
GACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAG  
10 ATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATCATTACTATGATAGT  
AGTGATTATCTCTACTACTACTACGGTTTGGACGTCTGGGGCCAAGGGACCAC  
GGTCACCGTCTCCTCAG (SEQ ID NO:73)

### B -- Cur2 1.33 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISA  
YNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDHYDSS  
DYLYYYYGLDVWGQGTTVTVSS (SEQ ID NO:31)

### 20 C -- Cur2 1.33 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGT  
ATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCAC  
25 TTTGCAATCAGGGGTCCCATCTCGGTTCAAGTGGCAGTGGATCTGGGACAGATT  
TCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGT  
CAAAAGTATAACAGTGCCCCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGA  
TCAAAC (SEQ ID NO:74)

### 30 D -- Cur2 1.33 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASLTQ  
SGVPSRFSGSGSGTDFTLTISLQPEDVATYYCQKYNAPLTFGGGTKVEIK (SEQ  
ID NO:32)

35

### FIGURE 13

A -- Cur2 1.38.1 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC  
TGAGACTCTCCTGTGCAGCGTCTGGATTACCTTCAGTAGCTATGGCATGCAC  
TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAATTATATGGT  
ATGATGGAAATGATAAATACTATGCAGACTCCGTGAAGGGCCGCTTCACCGT  
CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA  
10 GCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGATATTACTATGATAGTA  
GTGATTATCTCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCAC  
GGTCACCGTCTCCTCAG (SEQ ID NO:75)

B -- Cur2 1.38.1 heavy chain protein sequence

15 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAIIWY  
DGNDKYYADSVKGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCARGYYYDSS  
DYLYYYYGMDVWGQGTITVTVSS (SEQ ID NO:33)

20 C -- Cur2 1.38.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGT  
ATCAGCAGAAACCAGGGAAAGTTCCTAACCTCCTGATCTATGCTGCATCCAC  
25 TTTGCAATCAGGGGTCCCATCTCGGTTCAAGTGGCAGTGGATCTGGGACAGATT  
TCTCTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAGCTTATTACTGT  
CAAAAGTGTAACAGTGCCCCGTGGACGTTTCGGCCAAGGGACCACGGTGGAG  
ATCAAAC (SEQ ID NO:76)

30 D -- Cur2 1.38.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPNLLIYAASLTQ  
SGVPSRFSGSGSTDFSLTISSLQPEDVAAYYCQKCNSAPWTFGQGTVEIK (SEQ  
ID NO:34)

35



# FIGURE 14

## A -- Cur2 1.39.1 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCGGGAACAGAGGTGAAAAAGCCCGGGGAGTCT  
CTGAAGATCTCCTGTAAGGGTTCTGGATACAGGTTTACCAGCTACTGGATCGG  
CTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATCATCTAT  
CCTGGTGACTCTGATACCAGATAACAGCCCGTCCTTCCAAGGCCAGGTCACCA  
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA  
10 GGCTTCGGACACCGCCATGTATTACTGTGCGAGACATGGATCGTATTACTATA  
ATTCGGGGAGTTATTATAACGTCTTTGACTACTGGGGCCAGGGAACCCTGGTC  
ACCGTCTCCTCAG (SEQ ID NO:77)

## B -- Cur2 1.39.1 heavy chain protein sequence

15 EVQLVQSGTEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPG  
DSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYICARHGSYYNSGS  
YYNVFDYWGGTLVTVSS (SEQ ID NO:35)

## C -- Cur2 1.39.1 light chain nucleotide sequence

20 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG  
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA  
25 GTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGA  
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT  
GTCTACAGCATAATAGTTACCCGTGGACGTTTCGGCCAAGGGACCAAGGTGGA  
AATCAAAC (SEQ ID NO:78)

## D -- Cur2 1.39.1 light chain protein sequence

30 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ  
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ  
ID NO:36)

35

### **FIGURE 15**

A -- Cur2 1.40.1 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA  
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCACTTATGATATCAA  
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA  
CCCTAACAGTGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACC  
ATGACCAGGAACACCTCCCTAAGCACAGCCTACATGGAGCTGAGCAGCCTGA  
10 GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATATTGTAGTGGTGGT  
AGCTGCTACCAACTACTACAACGGTATGGACGTCTGGGGCCAAGGGACCACG  
GTCACCGTCTCCTCAG (SEQ ID NO:79)

B -- Cur2 1.40.1 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYDINWVRQATGQGLEWMGWM  
NPNSGNTGYAQKFQGRVTMTRNTSLSTAYMELSSLRSEDVAVYYCARDIVVVV  
AATNYINGMDVWVGQGTTVTVSS (SEQ ID NO:37)

20

## FIGURE 16

A -- Cur2 1.45 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA  
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAA  
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA  
CCCTAACAGTGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACC  
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA  
10 GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGCAGTGGATACAGCTA  
TGGTTACGACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTC  
ACCGTCTCCTCAG (SEQ ID NO:80)

B -- Cur2 1.45 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM  
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDNAVYYCARGSGYSYG  
YDYYYGMDVWGQGTITVTVSS (SEQ ID NO:38)

20 C -- Cur2 1.45 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCAATTGCCGGGCGAGTCAGGGCATTAGCAATGATTTAGCCTGG  
TATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCA  
25 CTTTGCAATTAGGGGTCCCATCTCGGTTTCAGTGGCAGTGGATCTGGGACAGAT  
TTCACCTCTACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTG  
TCAAAAGTATAACAGTGCCCCATTCACTTTCGGCCCTGGGACCAAAGTGGAT  
ATCAAAC (SEQ ID NO:81)

30 D -- Cur2 1.45 light chain protein sequence

DIQMTQSPSSLSASVGDRVTINCRASQGISNDLAWYQQKPGKVPKLLIYAASLTQ  
LGVPSRFSGSGSGTDFTLTISLQPEDVATYYCQKYNAPFTFGPGTKVDIK (SEQ  
ID NO:39)

35

## FIGURE 17

A -- Cur2 1.46.1 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA  
GTGAAGGTCTCCTGCAAGGCTTCTGGATACTCCTTCACCAGTTATGATATCAA  
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA  
CCCTAACAATGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACC  
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA  
10 GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATATTGTAGTGGTGGT  
AACTGCTACGGACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACG  
GTCACCGTCTCCTCAG (SEQ ID NO:82)

B -- Cur2 1.46.1 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSKASGYSFTSYDINWVRQATGQGLEWMGWM  
NPNNGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDNAVYYCARDIVVVVT  
ATDYYYGMDVWGQGTITVSS (SEQ ID NO:40)

20 C -- Cur2 1.46.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG  
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATTTTTGCTGCATCCA  
25 GTTTGCCAAGTGGGGTCCCATCAAGGTTCAAGCGGAGTGGATCTGGGACAGA  
ATTCATCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT  
GTCTACAGCATAGTGGTTACCCTCCGACGTTTCGGCCAAGGGACCAAGGTGGA  
AATCAAAC (SEQ ID NO:83)

30 D -- Cur2 1.46.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIFAASSLPS  
GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHSGYPPTFGQGGTKVEIK (SEQ ID  
NO:41)

35

## FIGURE 18

A -- Cur2 1.48.1 heavy chain nucleotide sequence

5 CAGGTTTCAGCTGGTGCAGTCGGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAG  
TGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGCTATGGTATCAGC  
TGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCG  
CTTACAATGGTAACACAACTATGCACAGAAGCTCCAGGGCAGAGTCACCAT  
GACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAG  
10 ATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATGTTGAATATTACTATG  
ATGGTAGTGGTTATTACTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACC  
GTCTCCTCAG (SEQ ID NO:84)

B -- Cur2 1.48.1 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISA  
YNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDVEYYD  
GSGYYYFDYWGGQGLTVTVSS (SEQ ID NO:42)

20 C -- Cur2 1.48.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGG  
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCA  
25 TTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGA  
TTTCACTCTCACCATCAGCAGCCTGCAGCCTGAGGATTTTGCATCTTACTATT  
GTCAACAGTCTAACAGTTTCCCTCGGACGTTTCGGCCAAGGGACCAAGGTGGA  
GATCAAAC (SEQ ID NO:85)

30 D -- Cur2 1.48.1 light chain protein sequence

DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASILQ  
SGVPSRFSGSGSGTDFTLTISLQPEDFASYCQQSNSFPRTFGQGTKVEIK (SEQ  
ID NO:43)

35

### **FIGURE 19**

A -- Cur2 1.49.1 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA  
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAA  
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA  
CCCTAACAGTGGTGACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACC  
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA  
10 GATCTGAGGACACGGCCGTGTATTTCTGTGCGAGAATGAGGGATATAGTGGC  
TACGAGCTATTACTACTACTTCTACGGTATGGACGTCTGGGGCCAAGGGACC  
ACGGTCACCGTCTCCTCAG (SEQ ID NO:86)

B -- Cur2 1.49.1 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWM  
NPNSGDTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYFCARMRDIVAT  
SYYYFYGMADVWGQGTTVTVSS (SEQ ID NO:44)

20 C -- Cur2 1.49.1 light chain nucleotide sequence

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCCGTCACCCCTGGAGAGCC  
GGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACA  
ACTATTTGGATTGGTACCTGCTGAAGCCAGGGCAGTCTCCACAGCTCCTGATC  
25 TATTTGGGTTCTAGTCGGGCCTCCGGGGTCCCTGACAGGTTCAGTGGCAGTGG  
ATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTT  
GGGGTTTATTACTGCATGCAAACCTCTACAAACTATCACCTTCGGCCAAGGGA  
CACGACTGGAGATTAAAC (SEQ ID NO:87)

30 D -- Cur2 1.49.1 light chain protein sequence

DIVMTQSPLSLPVTPGEPASISCRSSQSLLSNGYNYLDWYLLKPGQSPQLLIYLG  
SSRASGVPDFRFSGSGSGTDFTLKISRVEAEDVGVYYCMQTLQTITFGQGTRLEIK  
(SEQ ID NO:45)

35

## FIGURE 20

### A -- Cur2 1.51 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCGGGAGCTGAGGTGAAAAAGCCCCGGGGAGTCT  
CTGAAGATCTCCTGTAAGGGTTCTGGATACAGCTTTACCAGCTACTGGATCGG  
CTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATCATCTAT  
CCTGGTGACTCTGATGCCAAATACAGCCCGTCCTTCCAAGGCCAGGTCACCA  
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA  
10 GGCCTCGGACACCGCCATGTATTACTGTGCGAGACACTATGATTACGTTTGA  
GGAATTATCGGTATACAGGGTGGTTCGACCCCTGGGGCCAGGGAACCCTGGT  
CACCGTCTCCTCAG (SEQ ID NO:88)

### B -- Cur2 1.51.1 heavy chain protein sequence

15 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPG  
DSDAKYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMY YCARHYDYVWRNY  
RYTGWFDPWGQGT LVT VSS (SEQ ID NO:46)

### C -- Cur2 1.51.1 light chain nucleotide sequence

20 GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAG  
AGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCC  
TGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCAT  
25 CCAACAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGAC  
AGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATT  
ACTGTCAGCAGTATGGTAGCTCACTATTCACTTTCGGCCCTGGGACCAAAGTG  
GATATCAAAC (SEQ ID NO:89)

### D -- Cur2 1.51.1 light chain protein sequence

30 EIVLTQSPGTL SLSPGERATL SCRASQSVSSSYLAWYQQKPGQAPRL LIYGASNRA  
TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSLFTFGPGTKVDIK (SEQ  
ID NO:47)

35

## **FIGURE 21**

A -- Cur2 6.4 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAG  
TGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAAC  
TGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATAAAC  
CCTAATAGTGGTAACACAGACTATGCACAGAAGTTCCAGGGCAGAGTCACCA  
TGACCAGGGACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAG  
10 ATCTGAGGACACGGCCATATATTATTGTGTGAGAGGCTTTGGATACAGCTAT  
AATTACGACTACTATTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCA  
CCGTCTCCTCAGT (SEQ ID NO:90)

B -- Cur2 6.4 heavy chain amino acid sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWIN  
PNSGNTDYAQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNY  
DYYYGMDVWGQGTITVTVSS (SEQ ID NO:48)

C -- Cur2 6.4 light chain nucleotide sequence

20 GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAG  
AGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGTAGTAGTTACTTAGCCT  
GGTACCAGCAGAAGCCTGGCCAGGCTCCCAGGCTCCTCATCTATGCTACATC  
CAGCAGGGCCACTGGCATCCCAGACAGGTTCAAGTGGCAGTGGGTCTGGGACA  
GACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTA  
CTGTCAGCAGTATGGTAGTTCACCGTGCAGTTTGGCCAGGGGACCAAGCTG  
25 GAAATCAAGC (SEQ ID NO:91)

D -- Cur2 6.4 light chain amino acid sequence

30 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRA  
TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFQGQTKLEIK (SEQ  
ID NO:49)



**FIGURE 22A**

Clone	Germline genes used				No. of Nucleotide/ Amino acid changes						
					FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
CR2		V	D	J	V					D & J	
1.19.1	VH	V1-8	D3-16	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK2	0/0	0/0	0/0	0/0	1/1	1/1	0/0
6.4.1	VH	V1-8	D5-18	JH6B	0/0	0/0	0/0	3/2	5/3	0/0	0/0
	VK	A27		JK2	0/0	3/0	1/0	2/2	0/0	1/0	0/0
1.18	VH	V1-8	D6-19	JH6B	1/0	0/0	0/0	1/0	0/0	0/0	0/0
	VK	A30		JK3	0/0	0/0	0/0	0/0	1/1	0/0	0/0
1.40.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	mix									
1.45	VH	V1-8	DK4	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK3	1/1	1/1	0/0	1/1	0/0	0/0	0/0
1.46.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	A30		JK1	0/0	0/0	2/1	1/1	0/0	2/2	0/0
1.49.1	VH	V1-8	D5-12	JH6B	1/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A19		JK5	0/0	0/0	1/1	1/1	0/0	1/1	0/0
1.33	VH	V1-18	D21-9	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.48.1	VH	V1-18	D21-9	JH4B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	L5		JK1	0/0	0/0	0/0	1/1	2/1	1/1	0/0
1.6.1	VH	V3-21	D3-16	JH4B	0/0	4/4	0/0	1/1	1/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	1/1	0/0	0/0	0/0	0/0
1.17.1	VH	V3-33	D5-18	JH6B	2/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.24.1	VH	V3-33	D5-18	JH6B	0/0	2/1	0/0	1/1	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	1/0	0/0	0/0
1.38.1	VH	V3-33	D21-9	JH6B	1/0	0/0	0/0	3/3	2/1	0/0	0/0
	VK	A20		JK1	0/0	0/0	1/1	0/0	2/2	1/1	0/0
1.11.1	VH	V3-53	D4-17	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A19		JK4	0/0	1/1	0/0	0/0	0/0	0/0	0/0
1.23.1	VH	V5-51	D3-10	JH4B	1/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	1/1	1/1	0/0	0/0	0/0
1.25.1	VH	V5-51	D3-10	JH4B	1/0	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.29	VH	V5-51	D5-12	JH6B	1/0	0/0	0/0	0/0	1/1	0/0	0/0
	VK	A19		JK2	0/0	0/0	1/0	0/0	1/1	0/0	0/0
1.39.1	VH	V5-51	D3-10	JH4B	2/1	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.51.1	VH	5-51	D3-16	JH5B	2/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A27		JK3	0/0	0/0	0/0	1/1	0/0	0/0	0/0

**FIGURE 22B**

Clone	Germline genes used				No. of Nucleotide/ Amino acid changes						
					FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
CR2		V	D	J	V					D & J	
1.40.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	mix									
1.48.1	VH	V1-18	D21-9	JH4B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	L5		JK1	0/0	0/0	0/0	1/1	2/1	1/1	0/0
1.49.1	VH	V1-8	D5-12	JH6B	1/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A19		JK5	0/0	0/0	1/1	1/1	0/0	1/1	0/0
1.11.1	VH	V3-53	D4-17	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A19		JK4	0/0	1/1	0/0	0/0	0/0	0/0	0/0
1.29	VH	V5-51	D5-12	JH6B	1/0	0/0	0/0	0/0	1/1	0/0	0/0
	VK	A19		JK2	0/0	0/0	1/0	0/0	1/1	0/0	0/0
1.45	VH	V1-8	DK4	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK3	1/1	1/1	0/0	1/1	0/0	0/0	0/0
1.33	VH	V1-18	D21-9	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.38.1	VH	V3-33	D21-9	JH6B	1/0	0/0	0/0	3/3	2/1	0/0	0/0
	VK	A20		JK1	0/0	0/0	1/1	0/0	2/2	1/1	0/0
6.4.1	VH	V1-8	D5-18	JH6B	0/0	0/0	0/0	3/2	5/3	0/0	0/0
	VK	A27		JK2	0/0	3/0	1/0	2/2	0/0	1/0	0/0
1.51.1	VH	5-51	D3-16	JH5B	2/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A27		JK3	0/0	0/0	0/0	1/1	0/0	0/0	0/0
1.19.1	VH	V1-8	D3-16	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK2	0/0	0/0	0/0	0/0	1/1	1/1	0/0
1.18	VH	V1-8	D6-19	JH6B	1/0	0/0	0/0	1/0	0/0	0/0	0/0
	VK	A30		JK3	0/0	0/0	0/0	0/0	1/1	0/0	0/0
1.6.1	VH	V3-21	D3-16	JH4B	0/0	4/4	0/0	1/1	1/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	1/1	0/0	0/0	0/0	0/0
1.23.1	VH	V5-51	D3-10	JH4B	1/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	1/1	1/1	0/0	0/0	0/0
1.25.1	VH	V5-51	D3-10	JH4B	1/0	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.39.1	VH	V5-51	D3-10	JH4B	2/1	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.17.1	VH	V3-33	D5-18	JH6B	2/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.24.1	VH	V3-33	D5-18	JH6B	0/0	2/1	0/0	1/1	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	1/0	0/0	0/0
1.46.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	A30		JK1	0/0	0/0	2/1	1/1	0/0	2/2	0/0

**FIGURE 23**

**Figure 23A**

		Section 1					
	(1)	1	10	20	30	40	51
CUR2-1.6.1_HC	(1)	EVQLVESGGGLVKKPGGSLRLSCAASGPNFRITYNMNVVRQAPGKGLEWVSSI					
VH3-21	(1)	EVQLVESGGGLVKKPGGSLRLSCAASGFTFSYMNWVRQAPGKGLEWVSSI					
Consensus	(1)	EVQLVESGGGLVKKPGGSLRLSCAASGF F SY MNWVRQAPGKGLEWVSSI					
		Section 2					
	(52)	52	60	70	80	90	102
CUR2-1.6.1_HC	(52)	SSSSSNIIYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDIMI					
VH3-21	(52)	SSSSSYIYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR----					
Consensus	(52)	SSSSS IYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR					
		Section 3					
	(103)	103	110	126			
CUR2-1.6.1_HC	(103)	TFGGIIASFYFDYWGGTTLVTSS					
VH3-21	(99)	-----					
Consensus	(103)						

**Figure 23B**

		Section 1					
	(1)	1	10	20	30	40	51
CUR2-1.6.1_LC	(1)	DIQMTQSPSSLSASVGDRTTITCRASQGIRNDLGWFQQRPGKAPKRLIYAA					
A30	(1)	DIQMTQSPSSLSASVGDRTTITCRASQGIRNDLGWFQQRPGKAPKRLIYAA					
Consensus	(1)	DIQMTQSPSSLSASVGDRTTITCRASQGIRNDLGWFQQRPGKAPKRLIYAA					
		Section 2					
	(52)	52	60	70	80	90	102
CUR2-1.6.1_LC	(52)	SSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGT					
A30	(52)	SSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP-----					
Consensus	(52)	SSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP					
		Section 3					
	(103)	103	107				
CUR2-1.6.1_LC	(103)	KVEIK					
A30	(96)	-----					
Consensus	(103)						

## FIGURE 24

**Figure 24A**

								Section 1
	(1)	1	10	20	30	40	51	
Cur2-1.11.1_HC	(1)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI						
VH3-53	(1)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI						
Consensus	(1)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI						
								Section 2
	(52)	52	60	70	80	90	102	
Cur2-1.11.1_HC	(52)	YSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAGTVTTN						
VH3-53	(52)	YSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR-----						
Consensus	(52)	YSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCA						
								Section 3
	(103)	103	110	120				
Cur2-1.11.1_HC	(103)	YYYGMDVWGQGTITVTVSS						
VH3-53	(98)	-----						
Consensus	(103)							

**Figure 24B**

							Section 1
	(1)	1	10	20	30	40	51
CUR2-1.11.1_LC	(1)	DIVMTQSPLSLPVTTPGEPASISCRSSQSLLQSN GYN YLDWY LQKPGQSPQL					
A19	(1)	DIVMTQSPLSLPVTTPGEPASISCRSSQSLLHSN GYN YLDWY LQKPGQSPQL					
Consensus	(1)	DIVMTQSPLSLPVTTPGEPASISCRSSQSLL SNGYN YLDWY LQKPGQSPQL					
							Section 2
	(52)	52	60	70	80	90	102
CUR2-1.11.1_LC	(52)	LIYLGSNRASGV PDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTLTF					
A19	(52)	LIYLGSNRASGV PDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP--					
Consensus	(52)	LIYLGSNRASGV PDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQT					
							Section 3
	(103)	103	111				
CUR2-1.11.1_LC	(103)	GGGTKVEIK					
A19	(101)	-----					
Consensus	(103)						

**FIGURE 25**

**Figure 25A**

								Section 1	
	(1)	1	10	20	30	40	51		
CR2-1.17.1_HC	(1)	QVQLVESGGGVVQPGRSLRLSCAASGFTFS3YGMHWVRQAPGKGLEWVAVI							
VH3-33	(1)	QVQLVESGGGVVQPGRSLRLSCAASGFTFS3YGMHWVRQAPGKGLEWVAVI							
Consensus	(1)	QVQLVESGGGVVQPGRSLRLSCAASGFTFS3YGMHWVRQAPGKGLEWVAVI							
								Section 2	
	(52)	52	60	70	80	90	102		
CR2-1.17.1_HC	(52)	WYDGSNKYYADSVKGRFTISRDNSEKNTLYLQMNSLRAEDTAVYYCARDQGY							
VH3-33	(52)	WYDGSNKYYADSVKGRFTISRDNSEKNTLYLQMNSLRAEDTAVYYCAR----							
Consensus	(52)	WYDGSNKYYADSVKGRFTISRDNSEKNTLYLQMNSLRAEDTAVYYCAR							
								Section 3	
	(103)	103	110	126					
CR2-1.17.1_HC	(103)	RYAGYYDYGMDVWGQGTITVTVSS							
VH3-33	(99)	-----							
Consensus	(103)								

**Figure 25B**

							Section 1
	(1)	1	10	20	30	40	52
CR2-1.17.1_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPKGAPKRLIYAAS					
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPKGAPKRLIYAAS					
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPKGAPKRLIYAAS					
							Section 2
	(53)	53	60	70	80	90	104
CR2-1.17.1_LC	(53)	SLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHN8YPLTFGGGTV					
A30	(53)	SLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHN8YF-----					
Consensus	(53)	SLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHN8YP					
							Section 3
	(105)	1087					
CR2-1.17.1_LC	(105)	EIK					
A30	(96)	---					
Consensus	(105)						

**FIGURE 26**

**Figure 26A**

Section 1					
	(1)	10	20	30	40
CR2-1.18_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN			52
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN			
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN			
Section 2					
	(53)	53	60	70	80
CR2-1.18_HC	(53)	PNSGNTGYAQKFQGRVTMTTRNTSISTAYMELSSLRSED			104
VH1-8	(53)	PNSGNTGYAQKFQGRVTMTTRNTSISTAYMELSSLRSED			
Consensus	(53)	PNSGNTGYAQKFQGRVTMTTRNTSISTAYMELSSLRSED			
Section 3					
	(105)	105	110	126	
CR2-1.18_HC	(105)	GTYYYYYGMDVWGQGT			
VH1-8	(99)	-----			
Consensus	(105)				

**Figure 26B**

Section 1					
	(1)	10	20	30	40
CR2-1.18_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQRPGKAPKRLIYAASS			53
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQRPGKAPKRLIYAASS			
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQRPGKAPKRLIYAASS			
Section 2					
	(54)	54	60	70	80
CR2-1.18_LC	(54)	LQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYFCLQHNSYPFTFGPGTKVDI			106
A30	(54)	LQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYFCLQHNSYP-----			
Consensus	(54)	LQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYFCLQHNSYP			
Section 3					
	(107)	107			
CR2-1.18_LC	(107)	K			
A30	(96)	-			
Consensus	(107)				

Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

**Figure 27A**

	(1)	10	20	30	40	52	Section 1
Cur2-1.19.1_hc	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGGGLEWMGMWN					
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGGGLEWMGMWN					
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGGGLEWMGMWN					
	(53)	53	60	70	80	90	104
Cur2-1.19.1_hc	(53)	PNSGNTGYAQRPGQGRVTMTRNTSISTAYMELSSLRSED					
VH1-8	(53)	PNSGNTGYAQRPGQGRVTMTRNTSISTAYMELSSLRSED					
Consensus	(53)	PNSGNTGYAQRPGQGRVTMTRNTSISTAYMELSSLRSED					
	(105)	105	110	126			Section 3
Cur2-1.19.1_hc	(105)	GGVIVHYGMDVWGQGT					
VH1-8	(99)	-----					
Consensus	(105)						

**Figure 27B**

	(1)	10	20	30	40	52	Section 1
Cur2-1.19.1 Ic	(1) DIQMTQSPSSLSASVSGDRVTITCRASQGI	NDLGWYQQKPGKAPKRLIYAAS					
A30	(1) DIQMTQSPSSLSASVSGDRVTITCRASQGI	NDLGWYQQKPGKAPKRLIYAAS					
Consensus	(1) DIQMTQSPSSLSASVSGDRVTITCRASQGI	NDLGWYQQKPGKAPKRLIYAAS					
	(53)	53	60	70	80	90	104
Cur2-1.19.1 Ic	(53) SLQSGVPSRPSGSGSGTDFTLT	ISSLPQEDFATYYCLQHN	SDP	CSFGGQTKL			
A30	(53) SLQSGVPSRPSGSGSGTDFTLT	ISSLPQEDFATYYCLQHN	SDP	CSFGGQTKL			
Consensus	(53) SLQSGVPSRPSGSGSGTDFTLT	ISSLPQEDFATYYCLQHN	SDP	CSFGGQTKL			
	(105)	105	107				Section 3
Cur2-1.19.1 Ic	(105) EIR						
A30	(96) ---						
Consensus	(105)						

## FIGURE 28

**Figure 28A**

						Section 1
	(1)	1	10	20	30	40 51
Cur2-1.23.1_HC	(1)	EVQLVQSGAEVKKPGESLKISCEGSGYSFTSYWIGWVRQMPGKGLEWMGII				
VH5-51	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII				
Consensus	(1)	EVQLVQSGAEVKKPGESLKISC GSGYSFTSYWIGWVRQMPGKGLEWMGII				
						Section 2
	(52)	52	60	70	80	90 102
Cur2-1.23.1_HC	(52)	YPGDS DTRYSPSFQGGVTISADKSI STAYLQWSSLKASDTAMY YCARHVS Y				
VH5-51	(52)	YPGDS DTRYSPSFQGGVTISADKSI STAYLQWSSLKASDTAMY YCAR----				
Consensus	(52)	YPGDS DTRYSPSFQGGVTISADKSI STAYLQWSSLKASDTAMY YCAR				
						Section 3
	(103)	103	110	126		
Cur2-1.23.1_HC	(103)	YYVSGSYYNVFDYWGQGT LVT VSS				
VH5-51	(99)	-----				
Consensus	(103)					

**Figure 28B**

							Section 1
	(1)	1	10	20	30	40	51
Cur2-1.23.1_LC	(1)	DIQMTQSPSSLSASVGD RVTITCRASQGI RNDLGWYQQIPGRAPKRLIYAA					
A30	(1)	DIQMTQSPSSLSASVGD RVTITCRASQGI RNDLGWYQQKPGKAPKRLIYAA					
Consensus	(1)	DIQMTQSPSSLSASVGD RVTITCRASQGI RNDLGWYQQ PGRAPKRLIYAA					
							Section 2
	(52)	52	60	70	80	90	102
Cur2-1.23.1_LC	(52)	SSLQ RGVPSRFSGSGSGTEFTLTIS SLQPEDFATYYCLQHNSYPWTFGQGT					
A30	(52)	SSLQSGVPSRFSGSGSGTEFTLTIS SLQPEDFATYYCLQHNSYP-----					
Consensus	(52)	SSLQ GVP SRFSGSGSGTEFTLTIS SLQPEDFATYYCLQHNSYP					
							Section 3
	(103)	103	107				
Cur2-1.23.1_LC	(103)	KVEIK					
A30	(96)	-----					
Consensus	(103)						



## FIGURE 29

**Figure 29A**

								Section 1
	(1)	1	10	20	30	40	51	
CR2-1.24.1_HC	(1)	QVQLVESGGGVVQPGRSLRLSCAASGFTSFSSYGMHWVRQAPGKGLEWVADI						
VH3-33	(1)	QVQLVESGGGVVQPGRSLRLSCAASGFTSFSSYGMHWVRQAPGKGLEWVAVI						
Consensus	(1)	QVQLVESGGGVVQPGRSLRLSCAASGFTSFSSYGMHWVRQAPGKGLEWVA I						
								Section 2
	(52)	52	60	70	80	90	102	
CR2-1.24.1_HC	(52)	WYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQGY						
VH3-33	(52)	WYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR----						
Consensus	(52)	WYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR						
								Section 3
	(103)	103	110	126				
CR2-1.24.1_HC	(103)	SYGYVYYDYGMDVWGQGT TTVTS						
VH3-33	(99)	-----						
Consensus	(103)							

**Figure 29B**

Section 1							
	(1)	1	10	20	30	40	52
CR2-1.24.1 LC	(1)	DIQMTQSPSSLSASVGDRVTTITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS					
A30	(1)	DIQMTQSPSSLSASVGDRVTTITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS					
Consensus	(1)	DIQMTQSPSSLSASVGDRVTTITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS					
Section 2							
	(53)	53	60	70	80	90	104
CR2-1.24.1 LC	(53)	SLQSGVPSRFSGSGSGTEFTLTIS SLQPEDFATYYCLQHNSYPWTFGQGTKV					
A30	(53)	SLQSGVPSRFSGSGSGTEFTLTIS SLQPEDFATYYCLQHNSYP-----					
Consensus	(53)	SLQSGVPSRFSGSGSGTEFTLTIS SLQPEDFATYYCLQHNSYP					
Section 3							
	(105)	106	7				
CR2-1.24.1 LC	(105)	EIK					
A30	(96)	---					
Consensus	(105)						

# FIGURE 30

**Figure 30A**

		Section 1						
		(1)	1	10	20	30	40	51
VH5-51	(1)	EVQLVQSGAEVKKPQGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII						
CR2-1.25.1_HC	(1)	EVQLVQSGAEVKKPQGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGII						
Consensus	(1)	EVQLVQSGAEVKKPQGESLKISCKGSGY FTSYWIGWVRQMPGKGLEWMGII						
		Section 2						
		(52)	52	60	70	80	90	102
VH5-51	(52)	YFGDS DTRYSPSFQGGVTISADKSISTAYLQWSSLKASDTAMYYCAR----						
CR2-1.25.1_HC	(52)	YFGDS DTRYSPSFQGGVTISADKSISTAYLQWSSLKASDTAMYYCARHGSY						
Consensus	(52)	YFGDS DTRYSPSFQGGVTISADKSISTAYLQWSSLKASDTAMYYCAR						
		Section 3						
		(103)	103	110	126			
VH5-51	(99)	-----						
CR2-1.25.1_HC	(103)	YYGSEYYNVFDYWGQGLTVTVSS						
Consensus	(103)							

**Figure 30B**

Section 1						
	(1)	1	10	20	30	40 52
A30	(1)	DIQMTQSPSSLSASVGDRVTTTCRASQGIRNDLGWYQQKPKGKAPFRLIYAAS				
CR2-1.25.1_LC	(1)	DIQMTQSPSSLSASVGDRVTTTCRASQGIRNDLGWYQQKPKGKAPKRLIYAAS				
Consensus	(1)	DIQMTQSPSSLSASVGDRVTTTCRASQGIRNDLGWYQQKPKGKAPKRLIYAAS				
Section 2						
	(53)	53	60	70	80	90 104
A30	(53)	SLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYP-----				
CR2-1.25.1_LC	(53)	SLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGTKV				
Consensus	(53)	SLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYP				
Section 3						
	(105)	105	107			
A30	(96)	---				
CR2-1.25.1_LC	(105)	EIK				
Consensus	(105)					

## FIGURE 31

**Figure 31A**

								Section 1
	(1)	1	10	20	30	40	52	
VH5-51	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIYY						
CR2-1.29_HC	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIYY						
Consensus	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIYY						
								Section 2
	(53)	53	60	70	80	90	104	
VH5-51	(53)	FGDSDTRYSPSPFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR-----						
CR2-1.29_HC	(53)	FGDSDTRYSPSPFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGA						
Consensus	(53)	FGDSDTRYSPSPFQGGTISADKSISTAYLQWSSLKASDTAMYYCAR						
								Section 3
	(105)	105	110	129				
VH5-51	(99)	-----						
CR2-1.29_HC	(105)	TIGGYYYYYHGMDVWGQGTITVTVSS						
Consensus	(105)							

5

**Figure 31B**

								Section 1	
	(1)	1	10	20	30	40	53		
A19	(1)	DIVMTQSFLSLPVTGPGEFASISCRSSQSLHLSNGYNYLDWYLQKPGQSPQLLI							
CR2-1.29_LC	(1)	DIVMTQSFLSLPVTGPGEFASISCRSSQSLHLSNGYNYLDWYLQKPGQSPQLLI							
Consensus	(1)	DIVMTQSFLSLPVTGPGEFASISCRSSQSLHLSNGYNYLDWYLQKPGQSPQLLI							
								Section 2	
	(54)	54	60	70	80	90	106		
A19	(54)	YLGSNRASGVVDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPE-----							
CR2-1.29_LC	(54)	YLGSNRASGVVDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQSLMCSFGQ							
Consensus	(54)	YLGSNRASGVVDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQS							
								Section 3	
	(107)	107	113						
A19	(101)	-----							
CR2-1.29_LC	(107)	GTKLEIK							
Consensus	(107)								

10

**FIGURE 32**

***Figure 32A***

							Section 1
	(1)	1	10	20	30	40	52
VH1-18	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTSYGISWVRQAPGQGLEWMGWIS					
CR2-1.33_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTSYGISWVRQAPGQGLEWMGWIS					
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTSYGISWVRQAPGQGLEWMGWIS					
							Section 2
	(53)	53	60	70	80	90	104
VH1-18	(53)	AYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVVYCAR-----					
CR2-1.33_HC	(53)	AYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVVYCARDHYYDS					
Consensus	(53)	AYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVVYCAR					
							Section 3
	(105)	105	110	127			
VH1-18	(99)	-----					
CR2-1.33_HC	(105)	SDYLYYYYGLDVWGQGTTVTVSS					
Consensus	(105)						

***Figure 32B***

							Section 1
	(1)	1	10	20	30	40	53
A20	(1)	DIQMTQSPFSSLSASVGDRTTITCRASQGISNYLAWYQQKPGKVPKLLIYAAS					
CR2-1.33_LC	(1)	DIQMTQSPFSSLSASVGDRTTITCRASQGISNYLAWYQQKPGKVPKLLIYAAS					
Consensus	(1)	DIQMTQSPFSSLSASVGDRTTITCRASQGISNYLAWYQQKPGKVPKLLIYAAS					
							Section 2
	(54)	54	60	70	80	90	106
A20	(54)	LQSGVPSRFSGSGSGTDFTLTISLQPEDVATYYCQKYNAP-----					
CR2-1.33_LC	(54)	LQSGVPSRFSGSGSGTDFTLTISLQPEDVATYYCQKYNAPLTFGGGTKEI					
Consensus	(54)	LQSGVPSRFSGSGSGTDFTLTISLQPEDVATYYCQKYNAP					
							Section 3
	(107)	107					
A20	(96)	-					
CR2-1.33_LC	(107)	K					
Consensus	(107)						

# FIGURE 33

**Figure 33A**

		Section 1					
		(1)	10	20	30	40	51
VH3-33	(1)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAVI					
CR2-1.38.1_HC	(1)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAII					
Consensus	(1)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAII					
		Section 2					
		(52)	60	70	80	90	102
VH3-33	(52)	WYDGSNKYYADSVKGRFTISRDNSEKNTLYLQMNSLRAEDTAVYYCAR----					
CR2-1.38.1_HC	(52)	WYDGNCKYYADSVKGRFTISRDNSEKNTLYLQMNSLRAEDTAVYYCARGYYY					
Consensus	(52)	WYDG KYYADSVKGRFTISRDNSEKNTLYLQMNSLRAEDTAVYYCAR					
		Section 3					
		(103)	110	127			
VH3-33	(99)	-----					
CR2-1.38.1_HC	(103)	DSSDYLYYYYGMDVWGQGTITVTVSS					
Consensus	(103)						

**Figure 33B**

Section 1						
	(1)	10	20	30	40	52
A20	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQKPKGKVPKLLIYAAS				
CR2-1.38.1_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQKPKGKVPNLLIYAAS				
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQKPKGKVP LLIYAAS				
Section 2						
	(53)	60	70	80	90	104
A20	(53)	TLQSGVPSRFSGSGSGTDFTLTISLQPEDVATYYCQKYNAP-----				
CR2-1.38.1_LC	(53)	TLQSGVPSRFSGSGSGTDFTLTISLQPEDVAAYYCQKCNAPWTFGQGTIV				
Consensus	(53)	TLQSGVPSRFSGSGSGTDFTLTISLQPEDVA YYCQK NSAP				
Section 3						
	(105)	1067				
A20	(96)	---				
CR2-1.38.1_LC	(105)	EIK				
Consensus	(105)					

**FIGURE 34**

**Figure 34A**

								Section 1	
	(1)	1	10	20	30	40	51		
VH5-51	(1)	EVQLVQSGAEVKKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII							
CR2-1.39.1_HC	(1)	EVQLVQSGTEVKKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGII							
Consensus	(1)	EVQLVQSG EVKKKPGESLKISCKGSGY FTSYWIGWVRQMPGKGLEWMGII							
								Section 2	
	(52)	52	60	70	80	90	102		
VH5-51	(52)	YFGDS DTRYSPSFQGGQVTISADKSI STAYLQWSSLKASDTAMYYCAR----							
CR2-1.39.1_HC	(52)	YFGDS DTRYSPSFQGGQVTISADKSI STAYLQWSSLKASDTAMYYCARHGSY							
Consensus	(52)	YFGDS DTRYSPSFQGGQVTISADKSI STAYLQWSSLKASDTAMYYCAR							
								Section 3	
	(103)	103	110	126					
VH5-51	(99)	-----							
CR2-1.39.1_HC	(103)	YYNSG SYYNVFDYWGQGT LVTVSS							
Consensus	(103)								

**Figure 34B**

								Section 1		
	(1)	1	10	20	30	40	52			
A30	(1)	DIQMTQSPSSLSASVGDRTITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS								
CR2-1.39.1_LC	(1)	DIQMTQSPSSLSASVGDRTITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS								
Consensus	(1)	DIQMTQSPSSLSASVGDRTITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS								
								Section 2		
	(53)	53	60	70	80	90	104			
A30	(53)	SLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYP-----								
CR2-1.39.1_LC	(53)	SLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYFPTFGQGTKV								
Consensus	(53)	SLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYP								
								Section 3		
	(105)	1097								
A30	(96)	---								
CR2-1.39.1_LC	(105)	EIK								
Consensus	(105)									

**FIGURE 35**

**Figure 35A**

								Section 1	
	(1)	1	10	20	30	40	52		
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN							
CR2-1.45_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN							
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN							
								Section 2	
	(53)	53	60	70	80	90	104		
VH1-8	(53)	PNSGNTGYAQKFQGRVTMTNTSISTAYMELSSLRSEDVAVYYCAR-----							
CR2-1.45_HC	(53)	PNSGNTGYAQKFQGRVTMTNTSISTAYMELSSLRSEDVAVYYCARGSGYSY							
Consensus	(53)	PNSGNTGYAQKFQGRVTMTNTSISTAYMELSSLRSEDVAVYYCAR							
								Section 3	
	(105)	105	110	125					
VH1-8	(99)	-----							
CR2-1.45_HC	(105)	GYDYYYGMDVWGQGTITVTVSS							
Consensus	(105)								

5

**Figure 35B**

								Section 1	
	(1)	1	10	20	30	40	53		
A20	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAAS							
CR2-1.45_LC	(1)	DIQMTQSPSSLSASVGDRVTINCRASQGISNDLAWYQQKPGKVPKLLIYAAS							
Consensus	(1)	DIQMTQSPSSLSASVGDRVTI CRASQGISN LAWYQQKPGKVPKLLIYAAS							
								Section 2	
	(54)	54	60	70	80	90	106		
A20	(54)	LQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNAP-----							
CR2-1.45_LC	(54)	LQLGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNAPFTFGPGTKVDI							
Consensus	(54)	LQ GVPSPRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNAP							
								Section 3	
	(107)	107							
A20	(96)	-							
CR2-1.45_LC	(107)	K							
Consensus	(107)								

10

**FIGURE 36**

**Figure 36A**

							Section 1
	(1)	1	10	20	30	40	51
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGQGLEWMGWM					
CR2-1.46.1_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGQGLEWMGMM					
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGQGLEWMGWM					
							Section 2
	(52)	52	60	70	80	90	102
VH1-8	(52)	NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR----					
CR2-1.46.1_HC	(52)	NPNNGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDIVV					
Consensus	(52)	NPN GNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR					
							Section 3
	(103)	103	110	126			
VH1-8	(99)	-----					
CR2-1.46.1_HC	(103)	VVTATDYYYGMDVWGQGTTVTVSS					
Consensus	(103)						

**Figure 36B**

									Section 1
		(1)	1	10	20	30	40	52	
A30		(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYFAAS						
CR2-1.46.1_LC		(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIFAAS						
Consensus		(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIFAAS						
									Section 2
		(53)	53	60	70	80	90	104	
A30		(53)	SLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYP-----						
CR2-1.46.1_LC		(53)	SLP SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHSGYPPTFGQGTKV						
Consensus		(53)	SL SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQH YP						
									Section 3
		(105)	105	106	107				
A30		(96)	---						
CR2-1.46.1_LC		(105)	EIK						
Consensus		(105)							



**FIGURE 37**

**Figure 37A**

								Section 1	
	(1)	1	10	20	30	40	51		
CR2-1.48.1_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWI							
VH1-18	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWI							
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWI							
								Section 2	
	(52)	52	60	70	80	90	102		
CR2-1.48.1_HC	(52)	SAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDVEY							
VH1-18	(52)	SAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR----							
Consensus	(52)	SAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR							
								Section 3	
	(103)	103	110	125					
CR2-1.48.1_HC	(103)	YYDGSGLYYFDYWGQGLVTVSS							
VH1-18	(99)	-----							
Consensus	(103)								

**Figure 37B**

								Section 1
	(1)	1	10	20	30	40	52	
CR2-1.48.1_LC	(1)	DIQMTQSPSSVSASVGDRVTITCRASQGIS <del>SS</del> WLAWYQQKPGKAPKLLIYAAS						
L5	(1)	DIQMTQSPSSVSASVGDRVTITCRASQGIS <del>SS</del> WLAWYQQKPGKAPKLLIYAAS						
Consensus	(1)	DIQMTQSPSSVSASVGDRVTITCRASQGIS <del>SS</del> WLAWYQQKPGKAPKLLIYAAS						
								Section 2
	(53)	53	60	70	80	90	104	
CR2-1.48.1_LC	(53)	ILQSGVPSRFSGSGSGTDFTLTIS <del>SL</del> QPEDFASYYCQ <del>SN</del> SFPRTFGQGTKV						
L5	(53)	SLQSGVPSRFSGSGSGTDFTLTIS <del>SL</del> QPEDFATYYCQ <del>QANS</del> FP-----						
Consensus	(53)	LQSGVPSRFSGSGSGTDFTLTIS <del>SL</del> QPEDFASYYCQ <del>QANS</del> FP						
								Section 3
	(105)	105	107					
CR2-1.48.1_LC	(105)	EIK						
L5	(96)	---						
Consensus	(105)							

FIGURE 38

Figure 38A

								Section 1
	(1)	1	10	20	30	40	51	
CR2-1.49.1_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM						
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM						
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM						
								Section 2
	(52)	52	60	70	80	90	102	
CR2-1.49.1_HC	(52)	NPNSGDTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDVAVYFCARMRDI						
VH1-8	(52)	NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDVAVYFCAR----						
Consensus	(52)	NPNSG TGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDVAVYFCAR						
								Section 3
	(103)	103	110	127				
CR2-1.49.1_HC	(103)	VATSYYYYFYGMDVWGQGTTVTVSS						
VH1-8	(99)	-----						
Consensus	(103)							

Figure 38B

								Section 1			
	(1)	1	10	20	30	40	52				
CR2-1.49.1_LC	(1)	DIVMTQSPFLSLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLLKPGQSPQLL									
A19	(1)	DIVMTQSPFLSLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLLKPGQSPQLL									
Consensus	(1)	DIVMTQSPFLSLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLLKPGQSPQLL									
								Section 2			
	(53)	53	60	70	80	90	104				
CR2-1.49.1_LC	(53)	IYLGSSRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVVYCMQTLQTITFGQ									
A19	(53)	IYLGSSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVVYCMQALQTF----									
Consensus	(53)	IYLGSRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVVYCMQLQT									
								Section 3			
	(105)	105	111								
CR2-1.49.1_LC	(105)	GTRLEIK									
A19	(101)	-----									
Consensus	(105)										

**FIGURE 39**

**Figure 39A**

						Section 1
	(1)	1	10	20	30	40 51
CR2-1.51.1_HC	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII				
VH5-51	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII				
Consensus	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII				
						Section 2
	(52)	52	60	70	80	90 102
CR2-1.51.1_HC	(52)	YFGDSDAKYSPSFQGGQVTISADKSI STAYLQWSSLKASDTAMYYCARHYDY				
VH5-51	(52)	YFGDSDTRYSPSFQGGQVTISADKSI STAYLQWSSLKASDTAMYYCAR----				
Consensus	(52)	YFGDSD KYSPPSFQGGQVTISADKSI STAYLQWSSLKASDTAMYYCAR				
						Section 3
	(103)	103	110	126		
CR2-1.51.1_HC	(103)	VWRNYRYTGWFDPWGQGLTVTVSS				
VH5-51	(99)	-----				
Consensus	(103)					

5

**Figure 39B**

						Section 1
	(1)	1	10	20	30	40 52
CR2-1.51.1 LC	(1)	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGA				
A27	(1)	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGA				
Consensus	(1)	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGA				
						Section 2
	(53)	53	60	70	80	90 104
CR2-1.51.1 LC	(53)	SNRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGSSTLFTFGPGTK				
A27	(53)	SSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGSSTLFTFGPGTK				
Consensus	(53)	S RATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGSSTLFTFGPGTK				
						Section 3
	(105)	10908				
CR2-1.51.1 LC	(105)	VDIK				
A27	(97)	----				
Consensus	(105)					

10

**FIGURE 40**

**Figure 40A**

							Section 1
	(1)	1	10	20	30	40	52
Cur2-6.4.1_hc	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWIN					
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWIN					
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWIN					
							Section 2
	(53)	53	60	70	80	90	104
Cur2-6.4.1_hc	(53)	PNSGNTDYAQKFQGRVTMTTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSY					
VH1-8	(53)	PNSGNTGYAQKFQGRVTMTTRNTSISTAYMELSSLRSEDTAIYYCAR-----					
Consensus	(53)	PNSGNT YAQKFQGRVTMTR TSISTAYMELSSLRSEDTAIYYC R					
							Section 3
	(105)	105	110	125			
Cur2-6.4.1_hc	(105)	NYDYXYGMDVWGQGTTVTVSS					
VH1-8	(99)	-----					
Consensus	(105)						

5

**Figure 40B**

							Section 1
	(1)	1	10	20	30	40	52
Cur2-6.4.1_Lc	(1)	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYA					
A27	(1)	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGA					
Consensus	(1)	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYA					
							Section 2
	(53)	53	60	70	80	90	104
Cur2-6.4.1_Lc	(53)	SSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFQGGTK					
A27	(53)	SSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP-----					
Consensus	(53)	SSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP					
							Section 3
	(105)	105	108				
Cur2-6.4.1_Lc	(105)	LEIK					
A27	(97)	----					
Consensus	(105)						

10

**FIGURE 41**

CLONE #	VH	#DEL	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.19.1	DP-15/1-8	-1	CGAGAG (SEQ ID NO:92)	3	ACG	D3-16	28	TTATGATTACGTTT GGGGAGTTATCGT (SEQ ID NO:93)	2	GC	JH6 B	-12	ACTACG (SEQ ID NO:94)
1.19.2	DP-15/1-8	-1	CGAGAG (SEQ ID NO:92)	3	ACG	D3-16	28	TTATGATTACGTTT GGGGAGTTATCGT (SEQ ID NO:93)	2	GC	JH6 B	-12	ACTACG (SEQ ID NO:94)
1.19.3	DP-15/1-8	-1	CGAGAG (SEQ ID NO:92)	3	ACG	D3-16	28	TTATGATTACGTTT GGGGAGTTATCGT (SEQ ID NO:93)	2	GC	JH6 B	-12	ACTACG (SEQ ID NO:94)
6.4.1	DP-15/1-8	0	GAGAGG (SEQ ID NO:95)	3	CTT	D5-18	12	TGGATACAGCTA (SEQ ID NO:96)	2	TA	JH6 B	0	ATTACTAC (SEQ ID NO:97)
6.4.2	DP-15/1-8	0	GAGAGG (SEQ ID NO:95)	3	CTT	D5-18	12	TGGATACAGCTA (SEQ ID NO:96)	2	TA	JH6 B	0	ATTACTAC (SEQ ID NO:97)
6.4.3	DP-15/1-8	0	GAGAGG (SEQ ID NO:95)	3	CTT	D5-18	12	TGGATACAGCTA (SEQ ID NO:96)	2	TA	JH6 B	0	ATTACTAC (SEQ ID NO:97)

CLONE	vk	#del	vk end	#n	N SEQ	JK	# del	JK end
-------	----	------	--------	----	-------	----	-------	--------

1.19.1	A30	-3	TTACCC (SEQ ID NO:98)	6	GTGCAG (SEQ ID NO:99)	JK2	-7	TTTTGG (SEQ ID NO:100)
1.19.2	A30	-3	TTACCC (SEQ ID NO:98)	6	GTGCAG (SEQ ID NO:99)	JK2	-7	TTTTGG (SEQ ID NO:100)
1.19.3	A30	-3	TTACCC (SEQ ID NO:98)	6	GTGCAG (SEQ ID NO:99)	JK2	-7	TTTTGG (SEQ ID NO:100)
6.4.1	A27/A27A	-3	CTCACC (SEQ ID NO:99)	6	GTGCAG (SEQ ID NO:99)	JK2	-7	TTTTGG (SEQ ID NO:100)

# Table 1: Sequencing results

			NO:101)		NO:102)			NO:103)
6.4.2	A27/A27A	-3	CTCACC (SEQ ID NO:101)	6	GTGCAG (SEQ ID NO:102)	JK2	-7	TTTTGG (SEQ ID NO:103)
6.4.3	A27/A27A	-3	CTCACC (SEQ ID NO:101)	6	GTGCAG (SEQ ID NO:102)	JK2	-7	TTTTGG (SEQ ID NO:103)

**FIGURE 42**

CLONE #	VH	#DEL	VH END (SEQ ID NO:104)	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.6.1	DP-77/3-21	0	GAGAGA (SEQ ID NO:104)	0	0	D3-16	22	TATTATGATTAC GTTTGGGGA (SEQ ID NO:105)	14	ATTATCGCC TCGTT (SEQ ID NO:106)	JH4B	-1	CTACTT (SEQ ID NO:107)
1.6.1	DP-77/3-21	0	GAGAGA (SEQ ID NO:104)	0	0	D3-16	22	TATTATGATTAC GTTTGGGGA (SEQ ID NO:105)	14	ATTATCGCC TCGTT (SEQ ID NO:106)	JH4B	-1	CTACTT (SEQ ID NO:107)
1.6.1	DP-77/3-21	0	GAGAGA (SEQ ID NO:104)	0	0	D3-16	22	TATTATGATTAC GTTTGGGGA (SEQ ID NO:105)	14	ATTATCGCC TCGTT (SEQ ID NO:106)	JH4B	-1	CTACTT (SEQ ID NO:107)
1.11.1	DP-42/3-53	-5	AGAGA (SEQ ID NO:108)	3	GGA	D4-17	10	ACGGTGACTA (SEQ ID NO:109)	5	CGAAT (SEQ ID NO:110)	JH6B	-2	TACTACT A (SEQ ID NO:111)
1.11.2	DP-42/3-53	-5	AGAGA (SEQ ID NO:108)	3	GGA	D4-17	10	ACGGTGACTA (SEQ ID NO:109)	5	CGAAT (SEQ ID NO:110)	JH6B	-2	TACTACT A (SEQ ID NO:111)
1.23.1	DP-73/5-51	0	GAGACA (SEQ ID NO:112)	18	TGTATCGTATTACT ATGT (SEQ ID NO:113)	D3-10	19	TTCTGGGGAGTTA TTATAAC (SEQ ID NO:114)	2	GT	JH4B	-4	CTTTGA (SEQ ID NO:115)
1.23.2	DP-73/5-51	0	GAGACA (SEQ ID NO:112)	18	TGTATCGTATTACT ATGT (SEQ ID NO:113)	D3-10	19	TTCTGGGGAGTTA TTATAAC (SEQ ID NO:114)	2	GT	JH4B	-4	CTTTGA (SEQ ID NO:115)
CLONE	Vk	#del	vk end	#n	N SEQ	Jk	# del	JK end					
1.6.1	A30	-3	TTACCC (SEQ ID)	0	0	JK4	0	GCTCACT (SEQ ID)					

			NO:116)					NO:117)
1.6.2	A30	-3	TTACCC (SEQ ID NO:116)	0	0	JK4	0	GCTCACT (SEQ ID NO:117)
1.6.3	A30	-3	TTACCC (SEQ ID NO:116)	0	0	JK4	0	GCTCACT (SEQ ID NO:117)
1.11.1	A3/A19/DPK	-4	AAACTC (SEQ ID NO:118)	0	0	JK4	-2	TCACTTTC (SEQ ID NO:119)
1.11.2	A3/A19/DPK	-4	AAACTC (SEQ ID NO:118)	0	0	JK4	-2	TCACTTTC (SEQ ID NO:119)
1.23.1	A30	-3	TTACCC (SEQ ID NO:120)	0	0	JK1	0	GTGGAC (SEQ ID NO:120)
1.23.2	A30	-3	TTACCC (SEQ ID NO:120)	0	0	JK1	0	GTGGAC (SEQ ID NO:120)



**FIGURE 43**

CLONE #	VH	#DEL	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.17.1	DP-50/3-33	0	GAGAGA (SEQ ID NO:121)	4	TCAA	D5-18	8	GGATACA (SEQ ID NO:122)	9	ATATGCTG G (SEQ ID NO:123)	JH6B	-1	TTACTACT (SEQ ID NO:124)
1.17.2	DP-50/3-33	0	GAGAGA (SEQ ID NO:121)	4	TCAA	D5-18	8	GGATACA (SEQ ID NO:122)	9	ATATGCTG G (SEQ ID NO:123)	JH6B	-1	TTACTACT (SEQ ID NO:124)
1.17.3	DP-50/3-33	0	GAGAGA (SEQ ID NO:121)	4	TCAA	D5-18	8	GGATACA (SEQ ID NO:122)	9	ATATGCTG G (SEQ ID NO:123)	JH6B	-1	TTACTACT (SEQ ID NO:124)
1.18	DP-15/1-8	1	CGAGAG (SEQ ID NO:125)	1	A	D6-19	19	GGGTATAG CAGTGGCT GG (SEQ ID NO:126)	4	GACA	JH6B	-2	TACTAC (SEQ ID NO:127)
1.24.1	DP-50/3-33	0	GAGAGA (SEQ ID NO:128)	4	TCAG	DK4	18	GGATACAG CTATGGTT AC (SEQ ID NO:129)	2	GT	JH6B	-4	CTACTA (SEQ ID NO:130)
1.24.2	DP-50/3-33	0	GAGAGA (SEQ ID NO:128)	4	TCAG	DK4	18	GGATACAG CTATGGTT AC (SEQ ID NO:129)	2	GT	JH6B	-4	CTACTA (SEQ ID NO:130)
1.25.1	DP-73/5-51	0	GAGACA (SEQ ID NO:131)	6	TGGATC (SEQ ID NO:132)	D3-10	30	GTATATTA TGGTTCGG AGAcTTATT ATAA (SEQ ID NO:135)	3	TGT	JH4B	-4	CTTTGA (SEQ ID NO:135)

CLONE #	VH	#DEL	VH END (SEQ ID NO: )	# N's	N Sequence	DH	Size of D	D Sequence (SEQ ID NO: )	# N's	N Sequence	JH	# del	JH Segment (SEQ ID NO: )
1.25.2	DP-73/5-51	0	GAGACA (SEQ ID NO:131)	6	TGGATC (SEQ ID NO:132)	D3-10	30	GTATATTATA TGGTTCGG AGACTTATT ATAA (SEQ ID NO:133)	3	TGT	JH4B	-4	CTTTGA (SEQ ID NO:134)
1.29	DP-73/5-51	0	GAGACA (SEQ ID NO:135)	1	C	D5-12	21	GTGGATgT AGGGGCT ACGATT (SEQ ID NO:136)	7	GGGGAT (SEQ ID NO:137)	JH6B	0	ATTACTAC (SEQ ID NO:138)
1.33	DP-14/1-18	0	GAGAGA (SEQ ID NO:139)	2	TC	D21-9	18	ATTACTAT GATAGTAG TG (SEQ ID NO:140)	7	ATTATCT (SEQ ID NO:141)	JH6B	-4	CTACTA (SEQ ID NO:142)
1.38.1	DP-50/3-33	1	CGAGAG (SEQ ID NO:143)	2	GA	D21-9	19	TATTACTA TGATAGTA GTG (SEQ ID NO:144)	7	ATTATCT (SEQ ID NO:145)	JH6B	-4	CTACTA (SEQ ID NO:146)
1.39.1	DP-73/5-51	0	GAGACA (SEQ ID NO:147)	6	TGGATC (SEQ ID NO:148)	D3-10	31	GTATTACT ATAaTTCCG GGGAGTTA TTATAAC (SEQ ID NO:149)	2	GT	JH4B	-4	CTTTGA (SEQ ID NO:150)
1.39.2	DP-73/5-51	0	GAGACA (SEQ ID NO:147)	6	TGGATC (SEQ ID NO:148)	D3-10	31	GTATTACT ATAaTTCCG GGGAGTTA TTATAAC (SEQ ID NO:149)	2	GT	JH4B	-4	CTTTGA (SEQ ID NO:150)
1.40.1	DP-15/1-8	1	CGAGAG (SEQ ID NO:147)	0	0	D2	25	ATATTGTA GTGGTGGT	2	CA	JH6B	-6	ACTACT (SEQ ID NO:150)

ABX-Cur2 pat app.1

CLONE #	VH	#DEL	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
			NO:151)					AGCTGCTA C (SEQ ID NO:152)					NO:153)
1.40.2	DP-15/1-8	1	CGAGAG (SEQ ID NO:151)	0	0	D2	25	ATATTGTA GTGGTGGT AGCTGCTA C (SEQ ID NO:152)	2	CA	JH6B	-6	ACTACT (SEQ ID NO:153)
1.45	DP-15/1-8	0	GAGAGG (SEQ ID NO:154)	2	CA	DK4	20	GTGGATAC AGCTATGG TTAC (SEQ ID NO:155)	1	G	JH6B	-6	ACTACT (SEQ ID NO:156)
1.46.1	DP-15/1-8	1	CGAGAG (SEQ ID NO:157)	0	0	D2	25	ATATTGTA GT GGTGGTA GCTGCTAC (SEQ ID NO:158)	2	GG	JH6B	-6	ACTACT (SEQ ID NO:159)
1.46.2	DP-15/1-8	1	CGAGAG (SEQ ID NO:157)	0	0	D2	25	ATATTGTA GTGGTGGT AGCTGCTA C (SEQ ID NO:158)	2	GG	JH6B	-6	ACTACT (SEQ ID NO:159)
1.48.1	DP-14/1-18	1	CGAGAG (SEQ ID NO:160)	7	TGTTGAA (SEQ ID NO:161)	D21-9	20	TATTACTA TGATgGTA GTGGTTAT (SEQ ID NO:162)	1	T	JH4B	0	ACTACT (SEQ ID NO:163)
1.48.2	DP-14/1-18	1	CGAGAG (SEQ ID NO:160)	7	TGTTGAA (SEQ ID NO:161)	D21-9	20	TATTACTA TGATgGTA GTGGTTAT (SEQ ID NO:162)	1	T	JH4B	0	ACTACT (SEQ ID NO:163)

1.49.1 DP-15/1-8 2 GCGAGA (SEQ ID NO:164) 5 ATGAG (SEQ ID NO:165) D5-12 17 GGATATAG TGGCTACG A (SEQ ID NO:166) 3 GGATATAG TGGCTACG A (SEQ ID NO:166) NO:162) 0 ATTACTAC (SEQ ID NO:167) JH6B 0 ATTACTAC (SEQ ID NO:167)

CLONE #	VH	#DEL	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.49.1	DP-15/1-8	2	GCGAGA (SEQ ID NO:164)	5	ATGAG (SEQ ID NO:165)	D5-12	17	GGATATAG TGGCTACG A (SEQ ID NO:166)	3	GCT	JH6B	0	ATTACTAC (SEQ ID NO:167)
1.49.2	DP-15/1-8	2	GCGAGA (SEQ ID NO:164)	5	ATGAG (SEQ ID NO:165)	D5-12	17	GGATATAG TGGCTACG A (SEQ ID NO:166)	3	GCT	JH6B	0	ATTACTAC (SEQ ID NO:167)
1.51.1	DP-73/5-51	0	GAGACA (SEQ ID NO:168)	1	C	D3-16	31	TATGATTG CCGTTTGGa GGAaTTAT CCGGTATA (SEQ ID NO:169)	5	CAGGG (SEQ ID NO:170)	JH5B	-5	TGGTTC (SEQ ID NO:171)
1.51.2	DP-73/5-51	0	GAGACA (SEQ ID NO:168)	1	C	D3-16	31	TATGATTG CCGTTTGGa GGAaTTAT CCGGTATA (SEQ ID NO:169)	5	CAGGG (SEQ ID NO:170)	JH5B	-5	TGGTTC (SEQ ID NO:171)

CLONE	vk	#del	vk end	#n	N SEQ	Jk	# del	JK end
-------	----	------	--------	----	-------	----	-------	--------

1.17.1	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)
1.17.2	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)
1.17.3	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)

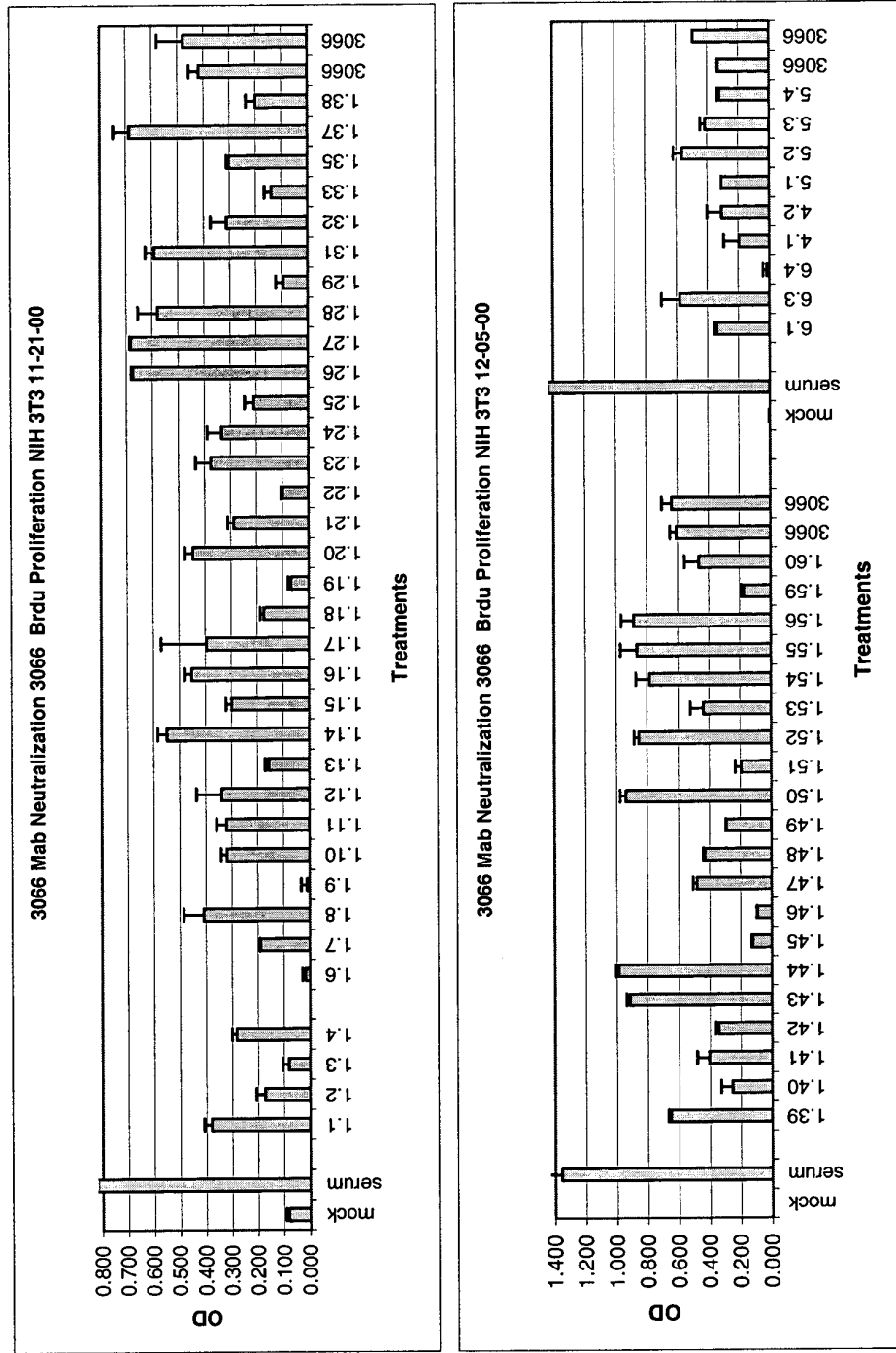
ABX-Cur2 pat app.1

CLONE	vk	#del	vk end	#n	N SEQ	JK	# del	JK end
			NO:172)					NO:173)
1.18	A30	3	TTACCC (SEQ ID NO:174)	0	0	JK3	0	ATTCAC (SEQ ID NO:175)
1.24.1	A30	3	TTACCC (SEQ ID NO:176)	0	0	JK1	0	GTGGAC (SEQ ID NO:177)
1.24.2	A30	3	TTACCC (SEQ ID NO:176)	0	0	JK1	0	GTGGAC (SEQ ID NO:177)
1.25.1	A30	3	TTACCC (SEQ ID NO:178)	0	0	JK1	0	GTGGAC (SEQ ID NO:179)
1.25.2	A30	3	TTACCC (SEQ ID NO:178)	0	0	JK1	0	GTGGAC (SEQ ID NO:179)
1.29	A3/A19/DPK	7	CTACAA (SEQ ID NO:180)	14	TCTCTCATG TGCAG (SEQ ID NO:181)	JK2	-7	TTTTGG (SEQ ID NO:182)
1.33	A20/DPK4	3	TGCCCC (SEQ ID NO:183)	0	0	JK4	0	GCTCAC (SEQ ID NO:184)
1.38.1	A20/DPK4	3	TGCCCC (SEQ ID NO:185)	0	0	JK1	0	GTGGAC (SEQ ID NO:186)
1.39.1	A30	3	TTACCC (SEQ ID NO:187)	0	0	JK1	0	GTGGAC (SEQ ID NO:188)
1.39.2	A30	3	TTACCC (SEQ ID NO:187)	0	0	JK1	0	GTGGAC (SEQ ID NO:188)
1.45	A20/DPK4	3	TGCCCC (SEQ ID NO:189)	0	0	JK3	0	ATTCAC (SEQ ID NO:190)
1.46.1	A30	0	CCCTCC (SEQ ID	0	0	JK1	-3	GACGTT (SEQ ID

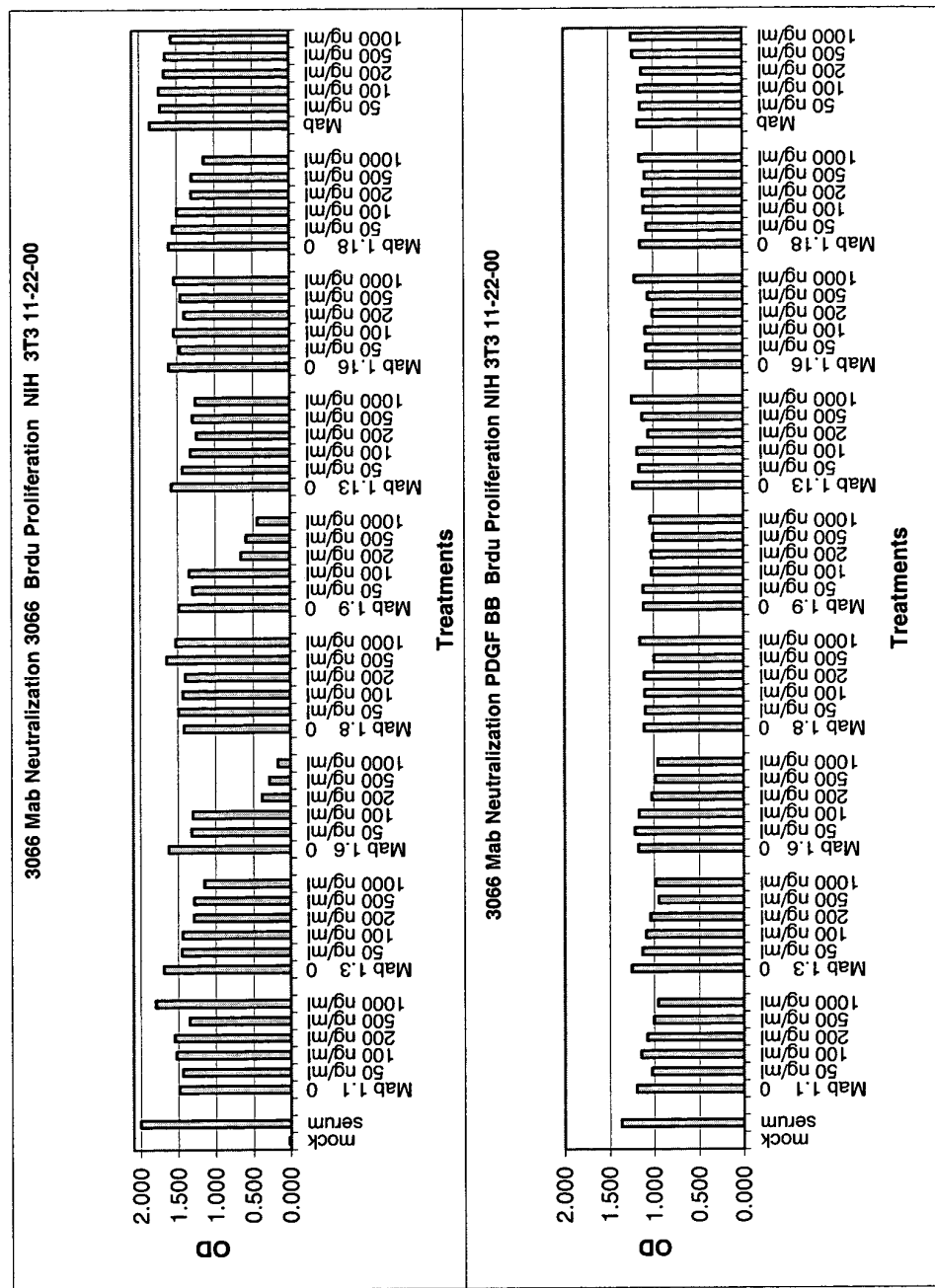
ABX-Cur2 pat app.1

CLONE	vk	#del	vk end	#n	N SEQ	JK	# del	JK end
			NO:191)					NO:192)
1.46.2	A30	0	CCCTCC (SEQ ID NO:191)	0	0	JK1	-3	GACGTT (SEQ ID NO:192)
1.48.1	L5/DPK5N	1	TCCCTC (SEQ ID NO:193)	0	0	JK1	-2	GGACGTT (SEQ ID NO:194)
1.48.2	L5/DPK5N	1	TCCCTC (SEQ ID NO:193)	0	0	JK1	-2	GGACGTT (SEQ ID NO:194)
1.49.1	A3/A19/DPK	5	CAAACT (SEQ ID NO:195)	0	0	JK5	-1	ATCACC (SEQ ID NO:196)
1.49.2	A3/A19/DPK	5	CAAACT (SEQ ID NO:195)	0	0	JK5	-1	ATCACC (SEQ ID NO:196)
1.51.1	A27/A27A	4	GCTCAC (SEQ ID NO:197)	1	T	JK3	0	ATTCAC (SEQ ID NO:198)
1.51.1	A27/A27A	4	GCTCAC (SEQ ID NO:197)	1	T	JK3	0	ATTCAC (SEQ ID NO:198)

**FIGURE 44**

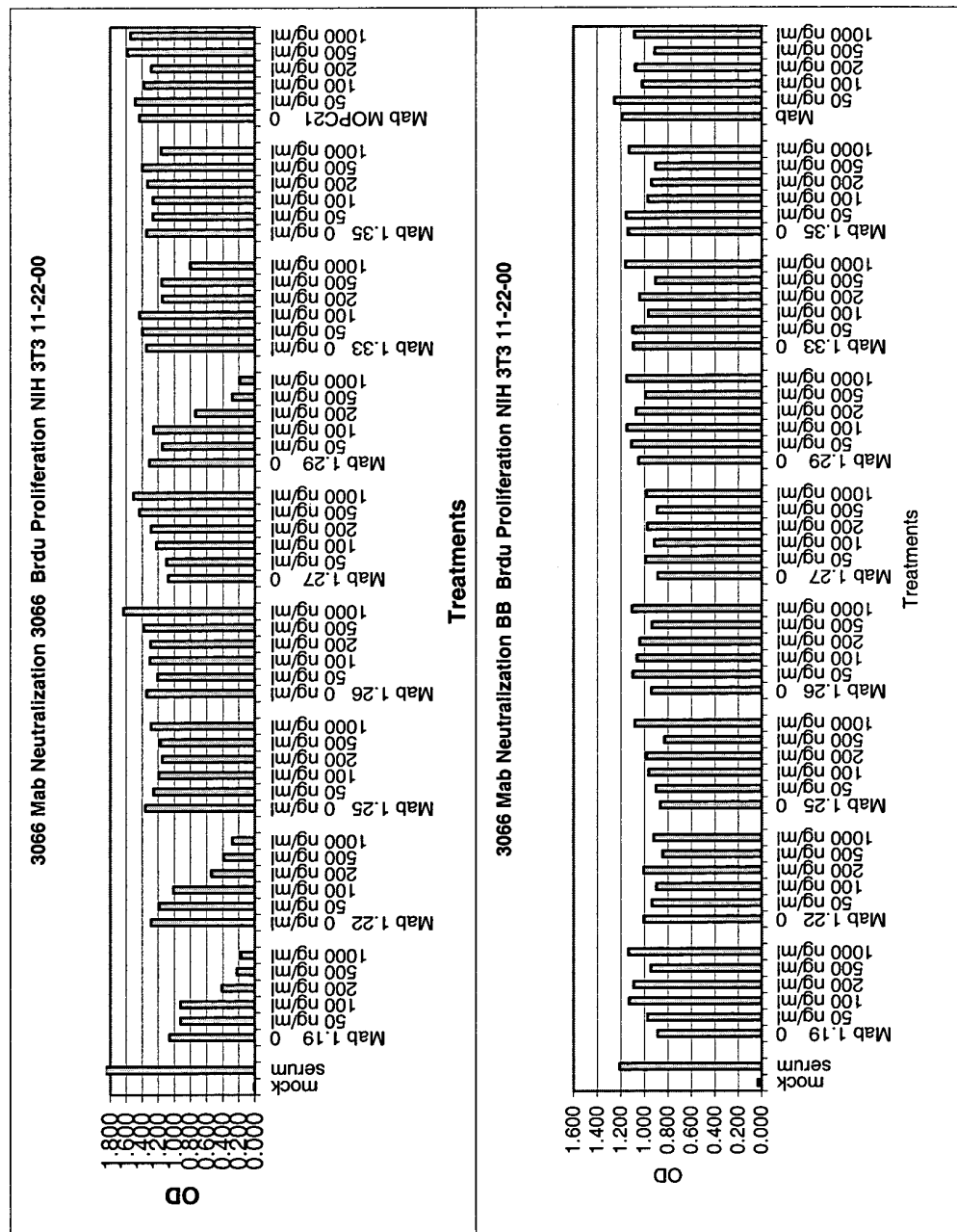


**FIGURE 45**

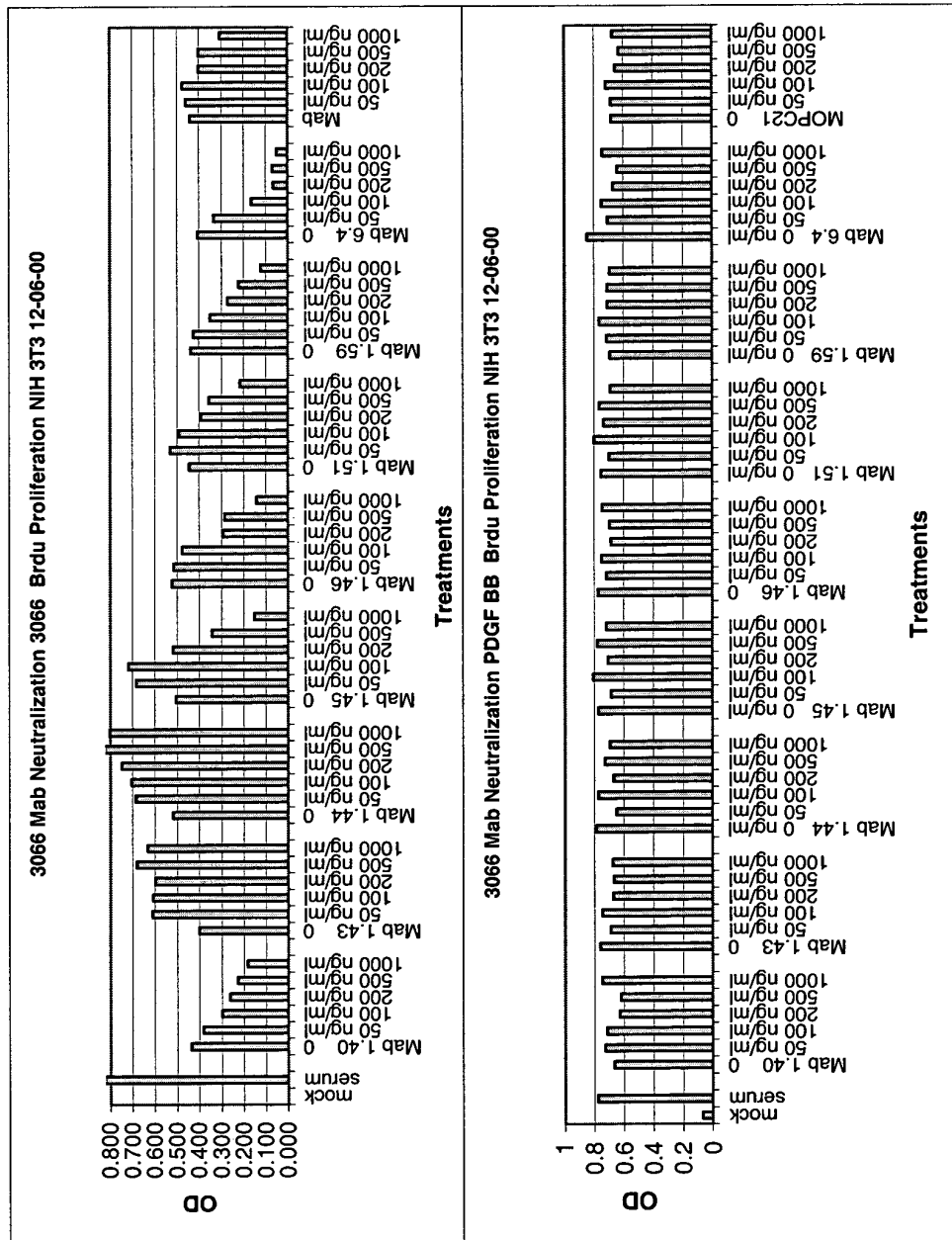




**FIGURE 46**



**FIGURE 47**



**FIGURE 48**

1.19 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
6.4 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY	60
1.18 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
1.40 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
1.45 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
1.46 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYSTFTSYDINWVRQATGQGLEWMGWMNPNGNTGY	60
1.49 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGDTGY	60
1.33 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY	60
1.48 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY	60
1.6 H	1	EVQLVESGGGLVKPGGSLRLISCAASCFNERTYNNWVRQAPGKGLEWVSSISSSSSNIYY	60
1.17 H	1	QVQLVESGGGVVQPGKSLRLISCAASCFTFSSYGMHWVRQAPGKGLEWVAWIWDGNSKYY	60
1.24 H	1	QVQLVESGGGVVQPGKSLRLISCAASCFSSYGMHWVRQAPGKGLEWVAWIWDGNSKYY	60
1.38 H	1	QVQLVESGGGVVQPGKSLRLISCAASCFTFSSYGMHWVRQAPGKGLEWVAWIWDGNDKYY	60
1.11 H	1	EVQLVQSGGGLIQPGGSLRLISCAASCFVSSNYMSWVRQAPGKGLEWVSVITSGGS-TYY	59
1.23 H	1	EVQLVQSGAEVKKPGESLKIISCEGSGYSFTSYWIGWVRQMPGKGLEWVGITYPGDSDTRY	60
1.25 H	1	EVQLVQSGAEVKKPGESLKIISCKGSGYRFTSYWIGWVRQMPGKGLEWVGITYPGDSDTRY	60
1.29 H	1	EVQLVQSGAEVKKPGESLKIISCKGSGYRFTSYWIGWVRQMPGKGLEWVGITYPGDSDTRY	60
1.39 H	1	EVQLVQSGTEVKKPGESLKIISCKGSGYRFTSYWIGWVRQMPGKGLEWVGITYPGDSDTRY	60
1.51 H	1	EVQLVQSGAEVKKPGESLKIISCKGSGYSFTSYWIGWVRQMPGKGLEWVGITYPGDSDAKY	60
		[ CDR1 ]	[ CDR2 ]
1.19 H	61	AQKFQGRVTMTTRNTSISTAYMELSSLRSEDNAVYYCAR--DVM-ITFGGVIVH-YGMDVW	116
6.4 H	61	AQKFQGRVTMTTRDTSISTAYMELSSLRSEDNAVYYCVR--GFG-YSYN-YDYY-YGMDVW	115
1.18 H	61	AQKFQGRVTMTTRNTSISTAYMELSSLRSEDNAVYYCAR--EG--IAVAGTYYYYYYGMDVW	116
1.40 H	61	AQKFQGRVTMTTRNTSLSTAYMELSSLRSEDNAVYYCAR--DIV-VVVAATNYY-NGMDVW	116
1.45 H	61	AQKFQGRVTMTTRNTSISTAYMELSSLRSEDNAVYYCAR--GSG-YSYG-YDYY-YGMDVW	115
1.46 H	61	AQKFQGRVTMTTRNTSISTAYMELSSLRSEDNAVYYCAR--DIV-VVVTATDYY-YGMDVW	116
1.49 H	61	AQKFQGRVTMTTRNTSISTAYMELSSLRSEDNAVYFCAR--MRD-IVATSYYYYFYGMDVW	117
1.33 H	61	AQKLOGRVTMTTDTSTSTAYMELRSLRSDDTNAVYYCAR--DHY-YDSSDYLYYYYGLDWW	117
1.48 H	61	AQKLOGRVTMTTDTSTSTAYMELRSLRSDDTNAVYYCARDVEYY-YDGSYYYFYEDY----W	115
1.6 H	61	ADSVKGRFTISRDNKNSLYLQMNLSLRAEDNAVYYCARDIMI---TFG-GIIASFYFDYW	116
1.17 H	61	ADSVKGRFTISRDNKNTLYLQMNLSLRAEDNAVYYCARDQGY---RYA-GYYYDYGMDVW	116
1.24 H	61	ADSVKGRFTISRDNKNTLYLQMNLSLRAEDNAVYYCARDQGY---SYG-YVYYDYGMDVW	116
1.38 H	61	ADSVKGRFTVSRDNKNTLYLQMNLSLRAEDNAVYYCARGYYD--SSD-YLYYYYGMDVW	117
1.11 H	60	ADSVKGRFTISRDNKNTLYLQMNLSLRAEDNAVYYCAGTVTT-----NYYYGMDVW	110
1.23 H	61	SPSFQGVVTSADKSIISTAYLQWSSLKASDTAMYYCARHVSY---YYVSGSY-NVFDYW	116
1.25 H	61	SPSFQGVVTSADKSIISTAYLQWSSLKASDTAMYYCARHGSY---YYGSETYY-NVFDYW	116
1.29 H	61	SPSFQGVVTSADKSIISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYY-HGMDVW	119
1.39 H	61	SPSFQGVVTSADKSIISTAYLQWSSLKASDTAMYYCARHGSY---YYNSGSY-NVFDYW	116
1.51 H	61	SPSFQGVVTSADKSIISTAYLQWSSLKASDTAMYYCARHYDY---VWRNYRYT-GWFDPW	116
		[ CDR3 ]	

**FIGURE 48 (CONT)**

1.19 H	117	GQGTIVTVSS	126
6.4 H	116	GQGTIVTVSS	125
1.18 H	117	GQGTIVTVSS	126
1.40 H	117	GQGTIVTVSS	126
1.45 H	116	GQGTIVTVSS	125
1.46 H	117	GQGTIVTVSS	126
1.49 H	118	GQGTIVTVSS	127
1.33 H	118	GQGTIVTVSS	127
1.48 H	116	GQGTIVTVSS	125
1.6 H	117	GQGTIVTVSS	126
1.17 H	117	GQGTIVTVSS	126
1.24 H	117	GQGTIVTVSS	126
1.38 H	118	GQGTIVTVSS	127
1.11 H	111	GQGTIVTVSS	120
1.23 H	117	GQGTIVTVSS	126
1.25 H	117	GQGTIVTVSS	126
1.29 H	120	GQGTIVTVSS	129
1.39 H	117	GQGTIVTVSS	126
1.51 H	117	GQGTIVTVSS	126

**FIGURE 49**

1.48 L	1	DIQMTQSPSSVSASVGDRVTTTCRASQGISS-----WLA	WYQQKPGKAPKLLIYAASITLQ	55
1.49 L	1	DIQMTQSPSLSLPVTIPGEPASISCRSSQSLH	SNNGYNLDWYLLKPGQSPQLLIYLGSSRA	60
1.11 L	1	DIQMTQSPSLSLPVTIPGEPASISCRSSQSLH	SNNGYNLDWYLLKPGQSPQLLIYLGSSRA	60
1.29 L	1	DIQMTQSPSLSLPVTIPGEPASISCRSSQSLH	SNNGYNLDWYLLKPGQSPQLLIYLGSSRA	60
1.45 L	1	DIQMTQSPSSLSASVGDRVTTTCRASQGISN----	DLAWYQQKPGKVPKLLIYAASITLQ	55
1.33 L	1	DIQMTQSPSSLSASVGDRVTTTCRASQGISN----	YLA	55
1.38 L	1	DIQMTQSPSSLSASVGDRVTTTCRASQGISN----	YLA	55
6.4 L	1	EIVLTQSPGTLISLSPGERATLSCRASQSVSSS----	YLA	56
1.51 L	1	EIVLTQSPGTLISLSPGERATLSCRASQSVSSS----	YLA	56
1.19 L	1	DIQMTQSPSSLSASVGDRVTTTCRASQGIRN----	DLG	55
1.18 L	1	DIQMTQSPSSLSASVGDRVTTTCRASQGIRN----	DLG	55
1.16 L	1	DIQMTQSPSSLSASVGDRVTTTCRASQGIRN----	DLG	55
1.23 L	1	DIQMTQSPSSLSASVGDRVTTTCRASQGIRN----	DLG	55
1.25 L	1	DIQMTQSPSSLSASVGDRVTTTCRASQGIRN----	DLG	55
1.39 L	1	DIQMTQSPSSLSASVGDRVTTTCRASQGIRN----	DLG	55
1.17 L	1	DIQMTQSPSSLSASVGDRVTTTCRASQGIRN----	DLG	55
1.24 L	1	DIQMTQSPSSLSASVGDRVTTTCRASQGIRN----	DLG	55
1.46 L	1	DIQMTQSPSSLSASVGDRVTTTCRASQGIRN----	DLG	55
		[ CDR1 ] [ CDR2 ]		
1.48 L	56	SGVPSRFGSGSGTDFTLTIS	SLQPEDFASY	107
1.49 L	61	SGVPDRFSGSGSGTDFTLTKIS	RV	111
1.11 L	61	SGVPDRFSGSGSGTDFTLTKIS	RV	111
1.29 L	61	SGVPDRFSGSGSGTDFTLTKIS	RV	113
1.45 L	56	LGVPSRFGSGSGSGTDFTLTIS	SLQPEDVAT	107
1.33 L	56	SGVPSRFGSGSGSGTDFTLTIS	SLQPEDVAT	107
1.38 L	56	SGVPSRFGSGSGSGTDFTLTIS	SLQPEDVAT	107
6.4 L	57	TGITPDRFSGSGSGTDFTLTIS	RL	108
1.51 L	57	TGITPDRFSGSGSGTDFTLTIS	RL	108
1.19 L	56	SGVPSRFGSGSGSGTDFTLTIS	SLQPEDFAT	107
1.18 L	56	SGVPSRFGSGSGSGTEFTLTIS	SLQPEDFAT	107
1.16 L	56	SGVPSRFGSGSGSGTEFTLTIS	SLQPEDFAT	107
1.23 L	56	RGVPSRFGSGSGSGTEFTLTIS	SLQPEDFAT	107
1.25 L	56	SGVPSRFGSGSGSGTEFTLTIS	SLQPEDFAT	107
1.39 L	56	SGVPSRFGSGSGSGTEFTLTIS	SLQPEDFAT	107
1.17 L	56	SGVPSRFGSGSGSGTEFTLTIS	SLQPEDFAT	107
1.24 L	56	SGVPSRFGSGSGSGTEFTLTIS	SLQPEDFAT	107
1.46 L	56	SGVPSRFGSGSGSGTEFTLTIS	SLQPEDFAT	107
		[ CDR3 ]		

**FIGURE 50**

1.19 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
6.4 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY	60
1.18 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
1.40 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
1.45 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
1.46 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNNCNTGY	60
1.49 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGDTGY	60

[ CDR1 ] [ CDR2 ]

1.19 H	61	AQKFQGRVTMTRNTSISTAYMELSSLRSEDNAVYYCARDVMITFGG-VIVHYGMDVWGQG	119
6.4 H	61	AQKFQGRVTMTRNTSISTAYMELSSLRSEDNAVYYVRGFGYSYN--YDYYYGMDVWGQG	118
1.18 H	61	AQKFQGRVTMTRNTSISTAYMELSSLRSEDNAVYYCAREGIAVAGT-YYYYYGMDVWGQG	119
1.40 H	61	AQKFQGRVTMTRNTSISTAYMELSSLRSEDNAVYYCARDIVVVVAA-TNYYNGMDVWGQG	119
1.45 H	61	AQKFQGRVTMTRNTSISTAYMELSSLRSEDNAVYYCARGSGYSYG--YDYYYGMDVWGQG	118
1.46 H	61	AQKFQGRVTMTRNTSISTAYMELSSLRSEDNAVYYCARDIVVVVTA-TDYYYGMDVWGQG	119
1.49 H	61	AQKFQGRVTMTRNTSISTAYMELSSLRSEDNAVYFCARMRDIVATSYYYYFYGMDVWGQG	120

[ CDR3 ]

1.19 H	120	TTVTVSS	126
6.4 H	119	TTVTVSS	125
1.18 H	120	TTVTVSS	126
1.40 H	120	TTVTVSS	126
1.45 H	119	TTVTVSS	125
1.46 H	120	TTVTVSS	126
1.49 H	121	TTVTVSS	127

**FIGURE 51**

<b>1.33 H</b>	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY	60
<b>1.48 H</b>	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY	60
		[____CDR1____]	[____CDR2____]
<b>1.33 H</b>	61	AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR--DHYYDSSDYLYYYYGLDVWG	118
<b>1.48 H</b>	61	AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDVEYYDGSGLYYFDY----WG	116
		_____]	[____CDR3____]
<b>1.33 H</b>	119	QGTITVTVSS	127
<b>1.48 H</b>	117	QGTITVTVSS	125

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY  
AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR--DHYYDSSDYLYYYYGLDVWG  
AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDVEYYDGSGLYYFDY----WG  
QGTITVTVSS  
QGTITVTVSS

**FIGURE 52**

1.17 H	1	QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVA	IWYDGSNKYY	60
1.24 H	1	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQAPGKGLEWVAD	IWYDGSNKYY	60
1.38 H	1	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVA	IWYDGNDKYY	60

[ CDR1 ] [ CDR2 ]

1.17 H	61	ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQGY	-RYAGY	YYDYGMDVWGQG	119
1.24 H	61	ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQGY	-SYGYV	YYDYGMDVWGQG	119
1.38 H	61	ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGYY	DSSDYLYYY	YGMDVWGQG	120

[ CDR3 ]

1.17 H	120	TTVTVSS	126
1.24 H	120	TTVTVSS	126
1.38 H	121	TTVTVSS	127

1.17 H 120 TTTTVSS 126  
1.24 H 120 TTTTVSS 126  
1.38 H 121 TTTTVSS 127



**FIGURE 53**

1.23	H	1	EVQLVQSGAEVKKPGESLKISCEGSGYSF	TSYWIGWVRQMPKGLEWMGIIYPGDS	TRY	60	
1.25	H	1	EVQLVQSGAEVKKPGESLKISCKGSGYR	TSYWIGWVRQMPKGLEWMGIIYPGDS	TRY	60	
1.29	H	1	EVQLVQSGAEVKKPGESLKISCKGSGYS	F	TSYWIGWVRQMPKGLEWMGIIYPGDS	TRY	60
1.39	H	1	EVQLVQSGTEVKKPGESLKISCKGSGYR	F	TSYWIGWVRQMPKGLEWMGIIYPGDS	TRY	60
1.51	H	1	EVQLVQSGAEVKKPGESLKISCKGSGYS	F	TSYWIGWVRQMPKGLEWMGIIYPGDS	DAKY	60

[\_\_\_CDR1\_\_\_]

[\_\_\_CDR2\_\_\_]

1.23	H	61	SPSFQGQVTISADKSISTAYLQWSSLKAS	TAMYYCARHVS	SYNVSG---	SYNVFDYWG	117
1.25	H	61	SPSFQGQVTISADKSISTAYLQWSSLKAS	TAMYYCARHGS	SYNVGSE---	TYNVFDYWG	117
1.29	H	61	SPSFQGQATISADKSISTAYLQWSSLKAS	TAMYYCARHVDVGATIG	GYHHGMDVWG	120	
1.39	H	61	SPSFQGQVTISADKSISTAYLQWSSLKAS	TAMYYCARHGS	SYNVNSG---	SYNVFDYWG	117
1.51	H	61	SPSFQGQVTISADKSISTAYLQWSSLKAS	TAMYYCARHYD	VWRNY---	RYTGWFDPWG	117

[\_\_\_CDR3\_\_\_]

1.23	H	118	QGTLVTVSS	126
1.25	H	118	QGTLVTVSS	126
1.29	H	121	QGTLVTVSS	129
1.39	H	118	QGTLVTVSS	126
1.51	H	118	QGTLVTVSS	126

**FIGURE 54**

<b>1.49 L</b>	<b>1</b>	DIVMTQSPLSLPVT	PGEPA	ISCRSSQSLLH	SNGYNYLDWYLL	KPGQSPQLLIYLGSSRA	60
<b>1.11 L</b>	<b>1</b>	DIVMTQSPLSLPVT	PGEPA	ISCRSSQSLLQ	SNGYNYLDWYLO	KPGQSPQLLIYLGSNRA	60
<b>1.29 L</b>	<b>1</b>	DIVMTQSPLSLPVT	PGEPA	ISCRSSQSLLH	SNGYNYLDWYLO	KPGQSPQLLIYLGSNRA	60
				[ CDR1 ]		[ CDR2 ]	
<b>1.49 L</b>	<b>61</b>	SGVPDRFSGSGSGTD	FTLKISRVEAED	DVG	VYYCMQTLQTTIT--	FGGTRLEIK	111
<b>1.11 L</b>	<b>61</b>	SGVPDRFSGSGSGTD	FTLKISRVEAED	DVG	VYYCMQALQTLT--	FGGTRKVEIK	111
<b>1.29 L</b>	<b>61</b>	SGVPDRFSGSGSGTD	FTLKISRVEAED	DVG	VYYCMQALQSLMCS	FGGTRKLEIK	113
				[ CDR3 ]			

1.49 L 1  
1.11 L 1  
1.29 L 1  
61  
61  
61

**FIGURE 55**

Accession	Length	CDR1	CDR2
1.45 L	1	DIQMTQSPSSLSASVGDRVIT	CRASQGISNDLAWYQQKPGKVPKLLIYAAS
1.33 L	1	DIQMTQSPSSLSASVGDRVIT	CRASQGISNQLAWYQQKPGKVPKLLIYAAS
1.38 L	1	DIQMTQSPSSLSASVGDRVIT	CRASQGISNQLAWYQQKPGKVPKLLIYAAS

<b>1.45 L</b>	61	RFSGSGSGTDFTLTIS	SSLQPEDVATYYCQKYNSAPFTFGP	GTKVDIK	107
<b>1.33 L</b>	61	RFSGSGSGTDFTLTIS	SSLQPEDVATYYCQKYNSAPLTF	CGGTKVEIK	107
<b>1.38 L</b>	61	RFSGSGSGTDFTSLTIS	SSLQPEDVAAYYCQKCN	SAPWTFGQGT	TVEIK 107

[ \_\_CDR3\_\_ ]

*(continued)*

**FIGURE 56**

<b>6.4 L</b>	1	EIVLTQSPGTL <del>SLSPGERATL</del> SCRASQSVSSSYLAWYQQKPGQAPRLLIYAT <del>SS</del> RATGIP	60
<b>1.51 L</b>	1	EIVLTQSPGTL <del>SLSPGERATL</del> SCRASQSVSSSYLAWYQQKPGQAPRLLIYGASNRATGIP	60
		[__CDR1__]	[_CDR2_]
<b>6.4 L</b>	61	DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPC <del>S</del> FGQGT <del>K</del> LEIK	108
<b>1.51 L</b>	61	DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSS <del>LF</del> TEGPGTKVDIK	108
		[__CDR3__]	

Sequence alignment of 6.4 L and 1.51 L antibody sequences. The alignment shows the variable regions of the heavy chain (L) and light chain (L) sequences. The sequences are aligned from position 1 to 108. The alignment shows that the sequences are highly similar, with only a few differences highlighted in the original image.

**FIGURE 57**

<b>1.19 L</b>	<b>1</b>	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
<b>1.18 L</b>	<b>1</b>	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
<b>1.16 L</b>	<b>1</b>	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
<b>1.23 L</b>	<b>1</b>	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
<b>1.25 L</b>	<b>1</b>	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
<b>1.39 L</b>	<b>1</b>	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
<b>1.17 L</b>	<b>1</b>	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
<b>1.24 L</b>	<b>1</b>	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
<b>1.46 L</b>	<b>1</b>	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60

[ \_\_\_CDR1\_\_\_] [ \_\_\_CDR2\_\_\_]

<b>1.19 L</b>	<b>61</b>	RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSDPESFGQGTKLEIR	107
<b>1.18 L</b>	<b>61</b>	RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPFTFGPGTKVDIK	107
<b>1.16 L</b>	<b>61</b>	RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK	107
<b>1.23 L</b>	<b>61</b>	RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGGGTKVEIK	107
<b>1.25 L</b>	<b>61</b>	RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGGGTKVEIK	107
<b>1.39 L</b>	<b>61</b>	RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGGGTKVEIK	107
<b>1.17 L</b>	<b>61</b>	RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK	107
<b>1.24 L</b>	<b>61</b>	RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGGGTKVEIK	107
<b>1.46 L</b>	<b>61</b>	RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPFTFGQGTKVEIK	107

[ \_\_\_CDR3\_\_\_]

1.19 L 1  
1.18 L 1  
1.16 L 1  
1.23 L 1  
1.25 L 1  
1.39 L 1  
1.17 L 1  
1.24 L 1  
1.46 L 1